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                     GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:          April 18, 2006, 12:06:40 ; Search time 9355.94 Seconds
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                               ALIGNMENTS

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DEFINITION  Sequence 7 from Patent WO0198482.
ACCESSION   AX379348
VERSION     AX379348.1  GI:19575188
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Miao,C.H. and Kay,M.A.
  TITLE     Liver-specific gene expression cassettes, and methods of use
  JOURNAL   Patent: WO 0198482-A 7 27-DEC-2001;
            The Board of Trustees of The Leland Stanford Junior University (US)
            ; The University of Washington (US)
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ORIGIN

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Db          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120

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Db        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420

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Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660

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Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Db       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
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Db       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707
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RESULT 2
CS098022
LOCUS       CS098022                38059 bp    DNA     linear   PAT 03-JUN-2005
DEFINITION  Sequence 4 from Patent WO2000075279.
ACCESSION   CS098022
VERSION     CS098022.1  GI:66954267
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kurachi,K. and Kurachi,S.
  TITLE     Nucleotide sequences for gene regulation and methods of use thereof
  JOURNAL   Patent: WO 2000075279-A 4 14-DEC-2000;
            The Regents of the University of Michigan (US)
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ORIGIN

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Qy          901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Qy          961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Qy         1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Qy         1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Qy         1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
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Qy         1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy         1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy         1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy         1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
                |||||||||||||||||||||  ||
Db        36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037


RESULT 3
AR390767
LOCUS       AR390767                38059 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6610906.
ACCESSION   AR390767
VERSION     AR390767.1  GI:40113109
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 38059)
  AUTHORS   Kurachi,K. and Kurachi,S.
  TITLE     Nucleotide sequences for gene regulation and methods of use thereof
  JOURNAL   Patent: US 6610906-A 4 26-AUG-2003;
            The Regents of the University of Michigan; Ann Arbor, MI
FEATURES             Location/Qualifiers
     source          1. .38059
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 1701.8;  DB 6;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy            1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy           61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy          121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy          181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy          241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037


RESULT 4
AX409478
LOCUS       AX409478                38059 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 2125 from Patent WO0229103.
ACCESSION   AX409478
VERSION     AX409478.1  GI:21442183
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE     Gene expression profiles in liver cancer
  JOURNAL   Patent: WO 0229103-A 2125 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1..38059
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. K02402"
ORIGIN

  Query Match             99.7%;  Score 1701.8;  DB 6;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
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Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
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Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
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Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037
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RESULT 5
HUMFIXG
LOCUS       HUMFIXG                38059 bp    DNA     linear   PRI 30-APR-1996
DEFINITION  Human coagulation factor IX gene, complete cds.
ACCESSION   K02402
VERSION     K02402.1  GI:182612
KEYWORDS    Alu repeat; Christmas factor; KpnI repetitive sequence;
            antihemophilic factor B; factor IX; repeat region; simple
            repetitive sequence.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 38059)
  AUTHORS   Yoshitake,S., Schach,B.G., Foster,D.C., Davie,E.W. and Kurachi,K.
  TITLE     Nucleotide sequence of the gene for human factor IX (antihemophilic
            factor B)
  JOURNAL   Biochemistry 24 (14), 3736-3750 (1985)
   PUBMED   2994716
REFERENCE   2  (bases 23487 to 23556)
  AUTHORS   Rees,D.J., Rizza,C.R. and Brownlee,G.G.
  TITLE     Haemophilia B caused by a point mutation in a donor splice junction
            of the human factor IX gene
  JOURNAL   Nature 316 (6029), 643-645 (1985)
   PUBMED   4033760
REFERENCE   3  (bases 23378 to 23387)
  AUTHORS   Graham,J.B., Lubahn,D.B., Lord,S.T., Kirshtein,J., Nilsson,I.M.,
            Wallmark,A., Ljung,R., Frazier,L.D., Ware,J.L., Lin,S.W.,
            Stafford,D.W. and Bosco,J.
  TITLE     The Malmo polymorphism of coagulation factor IX, an immunologic
            polymorphism due to dimorphism of residue 148 that is in linkage
            disequilibrium with two other F.IX polymorphisms
  JOURNAL   Am. J. Hum. Genet. 42 (4), 573-580 (1988)
   PUBMED   2450455
REFERENCE   4  (sites)
  AUTHORS   Hirosawa,S., Fahner,J.B., Salier,J.-P., Wu,C.-T., Lovrien,E. and
            Kurachi,K.
  TITLE     Structural and functional basis of the developmental regulation of
            human factor IX gene: factor IX Leyden
  JOURNAL   Unpublished (1990)
COMMENT     Original source text: Homo sapiens (clone:
            FIX-lambda-[6,36,53,61].) (tissue library: T.Maniatis et al.) DNA;
            and Homo sapiens (clone: FIX-lambda-4243) DNA.
            Sequence for [1] kindly submitted on floppy by K.Kurachi,
            05-AUG-1985.
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            [1] notes a potential TATA box (2939-2942) and polyadenylation
            signal (35701-35706); and notes two start codons (downstream of the
            start codon annotated below) that may be alternative and/or
            preferred starts for the factor IX prepropeptide.  Several tracts
            of simple repetitive sequence are present [1], including regions
            with the potential for hairpin and/or Z-DNA formation.  [1]
            describes six long open reading frames in the intron and on the
            complementary strand.
FEATURES             Location/Qualifiers
     source          1. .38059
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="Xq26.3-q27.1"
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Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
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RESULT 6
AF536327
LOCUS       AF536327               35458 bp    DNA     linear   PRI 21-AUG-2002
DEFINITION  Homo sapiens coagulation factor IX (plasma thromboplastic
            component, Christmas disease, hemophilia B) (F9) gene, complete
            cds.
ACCESSION   AF536327
VERSION     AF536327.1  GI:22385320
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 35458)
  AUTHORS   Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A.,
            Rajkumar,N.R., Toth,E.J., Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-2002) Genome Sciences, University of Washington,
            1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI HL66682 Program
            for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.gs.washington.edu).
FEATURES             Location/Qualifiers
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Db      32986 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 33045

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db      33286 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 33345

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db      33826 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 33885

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db      34126 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 34185

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
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Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
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RESULT 7
HS88D7
LOCUS       HS88D7                158557 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP6-88D7 on chromosome Xq25-26.3
            Contains the F9 gene for F9: coagulation factor IX (plasma
            thromboplastic component, Christmas disease, hemophilia B) (FIX,
            PTC, HEMB) and the 3' end of the  MCF2 gene for MCF.2 cell line
            derived transforming sequence (DBL), complete sequence.
ACCESSION   AL033403
VERSION     AL033403.1  GI:3859054
KEYWORDS    HTG; DBL; F9; FIX; HEMB; MCF2; PTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 158557)
  AUTHORS   Bird,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome X, constructed by the Sanger Centre Chromosome X Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX
            RP6-88D7 is from the library RPCI-6 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pPAC4
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
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  Matches 1699;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db      36227 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 36286

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db      36287 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 36346

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db      36347 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 36406
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Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Db      36407 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 36466

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Db      36467 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 36526

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db      36527 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 36586

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db      36587 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 36646

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Db      36647 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 36706

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36707 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 36766

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36767 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 36826

Qy       1441 TGATGATGCATGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
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Db      36827 TGATGATGCATGGACTACTGACAAAATCACTCTGACCCCGCCAAGCTGCTGCCTTCTCC 36886

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
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Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36947 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 37006

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37007 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 37066

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      37067 GAGGTTAGGAGTTTCAGGCCAGCCT 37091


RESULT 8
HUMFIXG6
LOCUS       HUMFIXG6                3121 bp    DNA     linear   PRI 01-DEC-1994
DEFINITION  Human factor IX gene, exons 7 and 8.
ACCESSION   K02053
VERSION     K02053.1  GI:182619
KEYWORDS    Christmas factor; factor IX.
SEGMENT     6 of 6
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3121)
  AUTHORS   Anson,D.S., Choo,K.H., Rees,D.J., Giannelli,F., Gould,K.,
            Huddleston,J.A. and Brownlee,G.G.
  TITLE     The gene structure of human anti-haemophilic factor IX
  JOURNAL   EMBO J. 3 (5), 1053-1060 (1984)
   PUBMED   6329734
REFERENCE   2  (bases 3011 to 3012; 3026 to 3028; 3090 to 3092)
  AUTHORS   Anson,D.S., Choo,K.H., Rees,D.J.G., Giannelli,F., Gould,K.,
            Huddleston,J.A. and Brownlee,G.G.
  JOURNAL   Unpublished (1985)
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COMMENT     Original source text: Human: cDNA to liver mRNA, clones cVII, cVI,
            108.1, and DB.1; 4X lymphoblastoid cell line (GM1416B) DNA, clone
            lambda-HIX-4; genomic DNA library of Lawn et al., clones
            lambda-HIX-1,2,3.
            [2]  revises [1].
            See segment 1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /map="Xq26.3-q27.1"
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                     K02052.1:82. .284,143. .257,926. .1473)
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                     /db_xref="GI:182621"
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                     YRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAEAVFPDVDYVNSTEAETILDNITQST
                     QSFNDFTRVVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKIT
                     VVAGEHNIEETEHTEQKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPI
                     CIADKEYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYN
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                     VNWIKEKTKLT"
     gene            join(K02048.1:325. .600,K02049.1:1. .599,K02050.1:1. .240,
                     K02051.1:1. .360,K02052.1:1. .360,1. .257)
                     /gene="F9"
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                     /note="fix mRNA"
     intron          <1. .142
                     /gene="F9"
                     /note="fix intron 6"
     exon            143. .257
                     /gene="F9"
                     /note="G00-119-900"
                     /number=7
     intron          258. .925
                     /note="fix intron 7"
     exon            926. .>1473
                     /note="factor IX"
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     old_sequence    3026. .3028
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     old_sequence    3090. .3092
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ORIGIN      About 9.96 kb after segment 5; chromosome Xq26.3-q27.2.

  Query Match             95.2%;  Score 1624.8;  DB 8;  Length 3121;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1642;  Conservative    0;  Mismatches    2;  Indels    6;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1472 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1531

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1532 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1591

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Db       1592 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1651

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1652 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1711
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Qy       241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Db      1712 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1771

Qy       301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1772 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1831

Qy       361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1832 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1891

Qy       421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1892 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1951

Qy       481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db      1952 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 2011

Qy       541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2012 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2071

Qy       601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2072 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2131

Qy       661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      2132 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGGGACTTGCTTTTCAGAACATAGGGA 2191

Qy       721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db      2192 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2251

Qy       781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db      2252 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2311

Qy       841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db      2312 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2371

Qy       901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      2372 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTGACGAAGGCAAGATTGGCAT 2431

Qy       961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db      2432 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2491

Qy      1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Db      2492 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2551

Qy      1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Db      2552 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2611

Qy      1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db      2612 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2671

Qy      1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Qy      1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Qy      1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Db      2792 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2851

Qy      1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
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Db      2852 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 2911

Qy      1441 TGATGATGCATGGGACTACTGACAAAATC------ACTCTGACCCTGCCAAGCTGCTGCC 1494
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Qy      1495 TTCTCCTGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTT 1554
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Qy      1555 TTAGTCAATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTT 1614
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Db      3032 TTAGTCAATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTT 3091

Qy      1615 GGCTGGGCCCAGTGGCTCACGCCTATAATC 1644
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Db      3092 GGCTGGGCCCAGTGGCTCACGCCTATAATC 3121


RESULT 9
AR178034
LOCUS       AR178034                2775 bp    DNA     linear   PAT 18-DEC-2001
DEFINITION  Sequence 22 from patent US 6315995.
ACCESSION   AR178034
VERSION     AR178034.1  GI:17920927
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2775)
  AUTHORS   Pinsky,D.J., Stern,D., Schmidt,A.Marie., Rose,E. and Solomon,R.A.
  TITLE     Methods for treating an ischemic disorder and improving stroke
            outcome
  JOURNAL   Patent: US 6315995-A 22 13-NOV-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             81.5%;  Score 1391;  DB 6;  Length 2775;
  Best Local Similarity   100.0%;  Pred. No. 2e-271;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db      1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy        61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db      1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy       121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Db      1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy       181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Qy       241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Qy       301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db      1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744
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Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db       1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db       1865 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1924

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Db       1925 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1984

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db       1985 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2285 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2344

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2404

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2405 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2464

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2524

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2525 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2584

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2585 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2704

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2764

Qy       1381 TTCTGGTTCAT 1391
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Db       2765 TTCTGGTTCAT 2775
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```
RESULT 10
HUMCIX
LOCUS       HUMCIX                  2775 bp    mRNA    linear   PRI 01-NOV-1994
DEFINITION  Human coagulation factor IX mRNA, complete cds.
ACCESSION   M11309
VERSION     M11309.1  GI:180552
KEYWORDS    clotting factor; clotting factor IX; coagulation factor;
            coagulation factor IX; factor IX.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2775)
  AUTHORS   McGraw,R.A., Davis,L.M., Noyes,C.M., Lundblad,R.L., Roberts,H.R.,
            Graham,J.B. and Stafford,D.W.
  TITLE     Evidence for a prevalent dimorphism in the activation peptide of
            human coagulation factor IX
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 82 (9), 2847-2851 (1985)
   PUBMED   3857619
REFERENCE   2  (bases 214 to 222; 313 to 321; 877 to 885)
  AUTHORS   Chen,S.H., Thompson,A.R., Zhang,M. and Scott,C.R.
  TITLE     Three point mutations in the factor IX genes of five hemophilia B
            patients. Identification strategy using localization by altered
            epitopes in their hemophilic proteins
  JOURNAL   J. Clin. Invest. 84 (1), 113-118 (1989)
   PUBMED   2472424
COMMENT     Original source text: Human liver cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .2775
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /map="Xq26.3-q27.1"
     gene            1. .2775
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                     /gene="F9"
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                     /codon_start=1
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                     YRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAETVFPDVDYVNSTEAETILDNITQST
                     QSFNDFTRVVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKIT
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                     CIADKEYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYN
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                     /gene="F9"
                     /note="coagulation factor IX signal peptide"
     mat_peptide     139. .573
                     /gene="F9"
                     /product="coagulation factor IX light chain"
     mat_peptide     574. .678
                     /gene="F9"
                     /product="coagulation factor IX activation peptide"
     mat_peptide     679. .1383
                     /gene="F9"
                     /product="coagulation factor IX heavy chain"
     variation       217
                     /gene="F9"
                     /note="g in wt; a in hemophilia Seattle 3 (Glu->Lys) [2]"
     variation       316
                     /gene="F9"
                     /note="g in wt; a in hemophilia Durham (Gly->Ser) [2]"
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     variation       580
                     /gene="F9"
                     /note="a in allele 1; g in allele 2 (Thr-> Ala)"
     variation       881
                     /gene="F9"
                     /note="g in wt; a in hemophilia Seattle 4 (Arg->Gln) [2]"
ORIGIN      Chromosome Xq26.3-q27.2.

  Query Match             81.5%;  Score 1391;  DB 8;  Length 2775;
  Best Local Similarity   100.0%;  Pred. No. 2e-271;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db       1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Db       1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Db       1565 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1624

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1684

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db       1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db       1865 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1924

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1925 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1984

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db       1985 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db       2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2225 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2284

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2285 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2344

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db       2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2404

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2405 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2464

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Db       2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2524

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db       2525 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2584

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2585 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2704

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2764

Qy       1381 TTCTGGTTCAT 1391
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Db       2765 TTCTGGTTCAT 2775


RESULT 11
G28615
LOCUS       G28615                  2775 bp    DNA     linear   STS 11-JUL-1996
DEFINITION  human STS SHGC-35785, sequence tagged site.
ACCESSION   G28615
VERSION     G28615.1  GI:1408430
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2775)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished (1996)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: GTAAGGTGCCTGAAAAGTTTGG
            Primer B: GTGAAATCATGCCTAGTCAGACC
            STS size: 219
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
```

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                Primer:          each 1 uM
                dNTPs:           each 200 uM
                Taq Polymerase:  0.05 units/ul
                Total Vol:       10 ul

           Buffer:
                MgCl2:           2.5 mM
                KCl:             50  mM
                Tris-HCl:        20  mM
                pH:              8.3

           Prepared with primer pairs provided by Sandoz, derived from M11309
           -- Washington University/Merck EST sequence.
FEATURES             Location/Qualifiers
     source          1..2775
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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     STS             2109..2327
     primer_bind     2109..2130
     primer_bind     complement(2305..2327)
ORIGIN

  Query Match             81.5%;  Score 1391;  DB 10;  Length 2775;
  Best Local Similarity   100.0%;  Pred. No. 2e-271;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db       1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db       1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Db       1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Db       1565 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1624

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Db       1625 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1684

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db       1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db       1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db       2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db       2225 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2284

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db       2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2404

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2405 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2464

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Db       2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2524

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db       2525 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2584

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db       2585 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2704

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2764

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2765 TTCTGGTTCAT 2775


RESULT 12
CQ882048
LOCUS       CQ882048                2804 bp    DNA     linear   PAT 11-OCT-2004
DEFINITION  Sequence 40 from Patent WO2004083404.
ACCESSION   CQ882048
VERSION     CQ882048.1  GI:54034760
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Qi,Y., Zhang,X. and Konigsberg,P.J.
  TITLE     Gene therapy vectors having reduced immunogenicity
  JOURNAL   Patent: WO 2004083404-A 40 30-SEP-2004;
            Isogenis, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..2804
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                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             81.5%;  Score 1391;  DB 6;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 2e-271;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db       1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db       1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Db       1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Db       1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db       1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db       1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Db       1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db       2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db       2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Db       2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db       2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2794 TTCTGGTTCAT 2804


RESULT 13
AR452580
LOCUS       AR452580                2804 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6677369.
ACCESSION   AR452580
VERSION     AR452580.1  GI:42684368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2804)
  AUTHORS   Beight,D.W., Craft,T.J., Franciskovich,J.B., Goodson,T. Jr.,
            Hall,S.E., Herron,D.K., Klimkowski,V.J., Masters,J.J., Mendel,D.,
            Milot,G., Sawyer,J.S., Shuman,R.T., Smith,G.F., Tebbe,A.L.,
            Tinsley,J.M., Weir,L.C., Wikel,J.H., Wiley,M.R. and Yee,Y.K.
  TITLE     Antithrombotic agents
  JOURNAL   Patent: US 6677369-A 2 13-JAN-2004;
            Eli Lilly and Company; Indianapolis, IN
FEATURES             Location/Qualifiers
     source          1..2804
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             81.5%;  Score 1391;  DB 6;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 2e-271;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db       1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
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Db       1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

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Db       1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db       2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Db       2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db       2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTCAT 1391
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Db       2794 TTCTGGTTCAT 2804


RESULT 14
A47227
LOCUS       A47227                  2802 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 1 from Patent WO9530000.
ACCESSION   A47227
VERSION     A47227.1  GI:2301257
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 2802)
  AUTHORS   Clark,A.J.
  TITLE     DNA SEQUENCES
  JOURNAL   Patent: WO 9530000-A 1 09-NOV-1995;
            BIOTECHNOLOGY AND BIOLOG SCIEN (GB)
COMMENT     Other publication AU 2317095 951129.
FEATURES             Location/Qualifiers
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                     /note="unnamed protein product"
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                     /db_xref="GI:2301258"
                     /translation="MQRVNMIMAESPGLITICLLGYLLSAECTVFLDHENANKILNRP
                     KRYNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNPC
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ORIGIN

  Query Match             81.2%;  Score 1385.8;  DB 6;  Length 2802;
  Best Local Similarity   99.9%;  Pred. No. 2.2e-270;
  Matches 1387;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db       1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db       1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

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Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db       1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db       1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTC 1389
              |||||||||
Db       2794 TTCTGGTTC 2802
```

```
RESULT 15
HSFACIXM
LOCUS       HSFACIXM                2781 bp    RNA     linear   PAT 02-MAR-1995
DEFINITION  H.sapiens factor IX mRNA.
ACCESSION   A22493
VERSION     A22493.1  GI:825655
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2781)
  AUTHORS   Brownlee,G.G. and Choo,K.H.
  TITLE     Molecular cloning of the gene for human anti-haemophilic factor IX
  JOURNAL   Patent: EP 0107278-A 15 02-MAY-1984;
            NATIONAL RESEARCH DEVELOPMENT CORPORATION
FEATURES             Location/Qualifiers
     source          1. .2781
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"
     gene            21. .1391
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     CDS             21. .1391
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                     /db_xref="GI:825656"
                     /translation="MIMAESPGLITICLLGYLLSAECTVFLDHENANKILNRPKRYNS
                     GKLEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNPCLNGGS
                     CKDDINSYECWCPFGFEGKNCELDVTCNIKNGTCEQFCKNSADNKVVCSCTEGYRLAE
                     NQKSCEPAVPFPCGRVSVSQTSKLTRAEAVFPDVDYVNSTEAETILDNITQSTQSFND
                     FTRVVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGE
                     HNIEETEHTEQKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADK
                     EYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYNNMFCA
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                     EKTKLT"
ORIGIN

  Query Match             81.2%;  Score 1385.6;  DB 6;  Length 2781;
  Best Local Similarity   99.7%;  Pred. No. 2.4e-270;
  Matches 1388;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1449

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1509

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1569

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1629

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1689

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1749

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1809
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Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1810 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1869

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1870 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1929

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1930 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1989

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        2050 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGGGACTTGCTTTTCAGAACATAGGGA 2109

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2110 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2169

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2170 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2229

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db        2230 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2289

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        2290 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTGACGAAGGCAAGATTGGCAT 2349

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db        2350 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2409

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        2410 TAATAATAATGCTAACAGAAAGAAGACAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2469

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2470 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2529

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2530 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2589

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2590 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2649

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2710 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2769

Qy        1381 TTCTGGTTCATA 1392
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                         GenCore version 5.1.7
                Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:03:10 ; Search time 1035.57 Seconds
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Searched:       4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:      9993994

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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                      %
Result                Query
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    1     1707   100.0   1707  6  AAI71008                  Aai71008 Human Fac
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    3   1701.8    99.7  38059  6  ABN95627                  Abn95627 Gene #212
    4   1701.8    99.7  38059 10   ADD71098                  Add71098 Human coa
    5     1391    81.5   2775  3  AAA54034                  Aaa54034 Human fac
    6     1391    81.5   2804  8  ABV77053                  Abv77053 Nucleotid
    7   1387.8    81.3   2792  2  AAX28626                  Aax28626 Nucleotid
    8   1385.6    81.2   2781  1  AAN40142                  Aan40142 Part of t
    9   1384.2    81.1   2802  2  AAT02460                  Aat02460 Human Fac
   10   1379.2    80.8   2781  1  AAN40177                  Aan40177 Part of t
   11   1376.6    80.6   2728 13   ADQ38340                  Adq38340 Human SNP
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   17     1292    75.7   2807  1  AAN60543                  Aan60543 Factor-IX
   18     1292    75.7   2807 12   ADH42198                  Adh42198 Novel hum
   19     1273    74.6   1273  4  AAF54017                  Aaf54017 hFIX gene
   20     1272    74.5   1272  4  AAF54080                  Aaf54080 hFIX gene
   21   1271.4    74.5   1273  4  AAF54074                  Aaf54074 hFIX gene
   22   1271.4    74.5   1273  4  AAF54073                  Aaf54073 hFIX gene
   23   1269.8    74.4   1273  4  AAF54075                  Aaf54075 hFIX gene
   24   1266.6    74.2   1273  4  AAF54076                  Aaf54076 hFIX gene
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   26     1261    73.9   1275  4  AAF54077                  Aaf54077 hFIX gene
   27     1260    73.8   1276  4  AAF54078                  Aaf54078 hFIX gene
   28    933.4    54.7   1971  4  ABA55251                  Aba55251 Human foe
   29    933.4    54.7   1971  4  ABS28575                  Abs28575 Human liv
   30      236    13.8   1438  6  ABQ82328                  Abq82328 Human NOV
   31      236    13.8   1438 12   ADH42196                  Adh42196 Novel hum
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   33      236    13.8   1639  1  AAN50049                  Aan50049 Sequence
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   36    200.6    11.8    201 13   ADQ40547                  Adq40547 Myocardia
   37    200.6    11.8    201 13   ADQ40266                  Adq40266 Myocardia
   38    200.6    11.8    201 13   ADQ40829                  Adq40829 Myocardia
   39    200.6    11.8    201 13   ADQ41116                  Adq41116 Myocardia
   40    172.4    10.1    422  8  ABX47596                  Abx47596 Bovine ES
   41      160     9.4   1610  2  AAX88061                  Aax88061 Human IGF
c  42      160     9.4  13928  4  AAH77500                  Aah77500 Haemophil
   43      159     9.3   1548  2  AAQ81549                  Aaq81549 Factor-IX
   44      159     9.3   1548  2  AAQ76017                  Aaq76017 Human Fac
   45      159     9.3   1548  2  AAX88292                  Aax88292 Human Fac

                                   ALIGNMENTS

RESULT 1
AAI71008
ID   AAI71008 standard; DNA; 1707 BP.
XX
AC   AAI71008;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human Factor IX gene 3' untranslated region.
XX
KW   Factor IX; human; expression cassette; liver; blood clotting;
KW   gene therapy; 3' untranslated region; 3' UTR; ds.
XX
OS   Homo sapiens.
XX
PN   WO200198482-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-US019634.
XX
PR   20-JUN-2000; 2000US-0212902P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Miao CH,  Kay MA;
XX
DR   WPI; 2002-114582/15.
XX
PT   Nucleic acid construct for expressing nucleic acid molecules, proteins in
PT   mammalian liver cells, has operably linked hepatic locus control element,
PT   hepatic promoter, coding sequence, polyadenylation signal and intron.
XX
PS   Example 1; Page 57-59; 64pp; English.
XX
CC   The present sequence is that of the 3' untranslated region (3' UTR) of
CC   the human Factor IX gene. The 3' UTR, which includes a polyadenylation
CC   signal. It was incorporated into expression cassettes of the invention
CC   that were designed for liver-specific expression of Factor IX. The
CC   cassettes also include an hepatic locus control element, an hepatic
CC   promoter located 3' to the hepatic locus control element, a Factor IX
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CC   coding sequence, and an intron (see AAI71003-16). Also provided are
CC   vectors that include an expression cassette of the invention. These may
CC   episomal or integrating vectors, including viral vectors, and are used in
CC   a claimed method of ameliorating disease. A therapeutic amount blood
CC   clotting Factor IX is produced in mammalian liver cells for at least 100
CC   days, and preferably at least 500 days. In examples of the invention,
CC   human Factor IX was expressed in mouse liver cells following injection of
CC   retrovirus-based plasmids that carried the expression cassettes into the
CC   tail vein or portal vein, and by direct injection of plasmid DNA into the
CC   liver
XX
SQ   Sequence 1707 BP; 500 A; 362 C; 305 G; 540 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1707;  DB 6;  Length 1707;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1707;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Db        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Db       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707
              |||||||||||||||||||||||||||
Db       1681 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707


RESULT 2
AAF54018
ID   AAF54018 standard; DNA; 38059 BP.
XX
AC   AAF54018;
XX
DT   30-MAR-2001  (first entry)
XX
DE   Human factor IX (hFIX) gene, SEQ ID NO:4.
XX
KW   Age-related gene regulation; liver-specific; gene expression;
KW   human factor IX; hFIX; AE5'; AE3'; age-regulatable expression construct;
```

```
KW   antisense therapy; gene therapy; thrombosis; cardiovascular disease;
KW   diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
KW   osteoarthritis; dementia; ds.
XX
OS   Homo sapiens.
XX
PN   WO200075279-A2.
XX
PD   14-DEC-2000.
XX
PF   06-JUN-2000; 2000WO-US015728.
XX
PR   09-JUN-1999;   99US-00328925.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Kurachi K,  Kurachi S;
XX
DR   WPI; 2001-061708/07.
DR   P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
DR   AAB60287, AAB60288, AAB60289.
XX
PT   New regulatory elements that control age-related gene expression, useful
PT   in gene therapy and for reducing Factor IX expression.
XX
PS   Disclosure; Fig 8A-B; 225pp; English.
XX
CC   The invention relates to nucleic acid sequences which regulate gene
CC   expression in an age-related manner and/or in a liver-specific manner.
CC   The invention identifies regions of the human factor IX (hFIX) gene, and
CC   a region of the human protein C (hPC) gene, which are age-related
CC   regulatory sequences. The hFIX age-related regulatory sequences are
CC   designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC   UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
CC   35655 of AAF54018) respectively. These elements act synergistically to
CC   increase hFIX levels over the lifespan of an individual; however, they
CC   can independently exert effects on hFIX mRNA in an age-related manner,
CC   with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
CC   mRNA levels, over time. AE5' also directs liver-specific expression. The
CC   hPC gene age-related regulatory sequence is found in the 5' UTR
CC   (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
CC   5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
CC   the invention, along with their homologues, variants and fragments, may
CC   be used in the construction of recombinant expression vectors for the
CC   expression of a desired sequence in an age-related fashion in a host
CC   cell. Preferred target genes for expression in such age-regulatable
CC   expression vectors include those encoding proteins involved in blood
CC   coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC   anti-coagulants protein C and antithrombin III), human alpha-1-
CC   antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
CC   Preferred promoters for use in such age-regulatable expression vectors
CC   include the human factor IX promoter, the T7 promoter, the T3 promoter
CC   and the SP6 promoter. The expression vectors of the invention may be used
CC   in gene therapy to provide age- related and/or liver-specific expression
CC   of target genes. Age-regulatable constructs may be used in the treatment
CC   of such age-related conditions such as thrombosis, cardiovascular
CC   disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
CC   osteoporosis, osteoarthritis and dementia. Specifically, they may be used
CC   to express factor IX antisense mRNA in the treatment of thrombotic
CC   conditions associated with the natural age-related rise in factor IX
CC   expression. Transgenic cells or animals that contain vectors of the
CC   invention are useful as models of these diseases, in screening for
CC   potential therapeutic agents and for studying normal processes such as
CC   ageing and gene expression. Fragments and homologues of age-related
CC   regulatory sequences, are useful as probes to detect, isolate or identify
CC   other such sequences in samples. The present sequence represents the hFIX
CC   gene
XX
SQ   Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1701.8;  DB 4;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412
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Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037


RESULT 3
ABN95627
ID   ABN95627 standard; DNA; 38059 BP.
XX
AC   ABN95627;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Gene #2125 used to diagnose liver cancer.
XX
KW   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW   metastatic liver tumour; cytostatic; expression profile; disease state;
KW   disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS   Homo sapiens.
XX
PN   WO200229103-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030589.
XX
PR   02-OCT-2000; 2000US-0237054P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Horne D,  Alvares C,  Peres-Da-Silva S,  Vockley JG;
XX
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DR   WPI; 2002-426119/45.
XX
PT   Diagnosing and detecting the progression of liver cancer, hepatocellular
PT   carcinoma or metastatic liver tumor in a patient, involves detecting the
PT   level of expression of two or more genes in a liver tissue sample.
XX
PS   Claim 1; SEQ ID NO 2125; 298pp; English.
XX
CC   The invention relates to a novel method for diagnosing and detecting the
CC   progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC   tumour in a patient, and differentiating metastatic liver cancer from
CC   hepatocellular carcinoma in a patient, involving detecting the level of
CC   expression of two or more genes represented in ABN93503-ABN97455 in a
CC   tissue sample. The method of the invention has hepatotropic, and
CC   cytostatic activity. The method is useful for diagnosing and detecting
CC   the progression of liver cancer, hepatocellular carcinoma and metastatic
CC   liver carcinoma in a patient. The method is useful for identifying
CC   expression profiles which serve as useful diagnostic markers as well as
CC   markers that can be used to monitor disease states, disease progression,
CC   drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1701.8;  DB 6;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992
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Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037
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RESULT 4
ADD71098
ID   ADD71098 standard; DNA; 38059 BP.
XX
AC   ADD71098;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human coagulation factor IX gene SEQ ID NO:102.
XX
KW   liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic;
KW   cytostatic; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003061564-A2.
XX
PD   31-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-US040718.
XX
PR   21-DEC-2001; 2001US-0341815P.
PR   31-DEC-2001; 2001US-0343185P.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (LGBI-) LG BIOMEDICAL INST.
XX
PI   Koh SS,  Liu Q,  Chung H,  Zeng W,  Lee B,  Yeramilli S,  Song SY;
XX
DR   WPI; 2003-663343/62.
XX
PT   Diagnosing liver cancer cells, useful for treating liver cancer
PT   associated with chronic hepatitis or cirrhosis comprises detecting the
PT   level of expression in a tissue sample of one or more genes associated
PT   with cancerous liver tissues.
XX
PS   Claim 1; SEQ ID NO 102; 176pp; English.
XX
CC   The present invention describes a method for diagnosing liver cancer
CC   cells comprising detecting the level of expression in a tissue sample of
CC   one or more genes given in the specification (see ADD70997 to ADD71105),
CC   where differential expression of the genes is indicative of liver cancer.
CC   Also described: (1) detecting the progression of liver cancer in a
CC   patient; (2) monitoring the treatment of a patient with liver cancer; (3)
CC   treating a patient with liver cancer; (4) typing a liver disease in a
CC   patient; (5) detecting the presence or progression of liver cancer in a
CC   patient with chronic hepatitis or cirrhosis; (6) differentiating liver
CC   cancer related to chronic hepatitis from liver cancer related to
CC   cirrhosis; (7) screening for an agent capable of modulating the onset or
CC   progression of liver cancer; (8) a composition comprising at least two
CC   oligonucleotides comprising a sequence that specifically hybridises to
CC   any of the genes; (9) a solid support comprising the at least two
CC   oligonucleotides; (10) a computer system comprising a database containing
CC   information identifying the level in liver tissue of a set of genes; (11)
CC   a method for using the computer system to present information identifying
CC   the expression level in tissue or cell of any of the genes; and (12) a
CC   therapeutic agent for slowing or halting the progression of liver cancer.
CC   The methods are useful for treating liver cancer associated with chronic
CC   hepatitis or cirrhosis. The present sequence represents a specifically
CC   claimed human gene sequence which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1701.8;  DB 10;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392
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Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037


RESULT 5
AAA54034
ID   AAA54034 standard; DNA; 2775 BP.
XX
AC   AAA54034;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human factor IX coding sequence.
XX
KW   Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein;
KW   fusion protein; coagulation factor; Factor X; Factor VII; Protein S;
KW   Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200054787-A1.
XX
PD   21-SEP-2000.
XX
PF   16-MAR-2000; 2000WO-US006934.
XX
PR   16-MAR-1999;   99US-0124609P.
XX
PA   (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   High KA,  Camire RM,  Larson PJ,  Stafford DW;
XX
DR   WPI; 2000-638152/61.
XX
PT   Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent
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PT   protein useful for treating diseases associated with the protein,
PT   comprises sequence encoding propeptide fused to sequence encoding the
PT   protein.
XX
PS   Disclosure; Fig 6Di-ii; 60pp; English.
XX
CC   Efficient processing and release of mature two-chain factor X into the
CC   circulation requires: removal of the signal sequence; formation of
CC   disulfide bonds; modification of amino terminal glutamic acid residues,
CC   to gamma-carboxyglutamic acid; modification of one aspartic acid in the
CC   first epidermal growth factor (EGF) domain to Beta-hydroxyaspartic acid;
CC   addition of N- and O-linked oligosaccharides to the activation peptide;
CC   removal of an internal tripeptide to yield two-chain factor X and removal
CC   of the propeptide just prior to secretion. While some of these
CC   modifications do not appear essential for factor X function the removal
CC   of the signal sequence, propeptide, internal tripeptide and full gamma-
CC   carboxylation are all steps which are important requisites for the
CC   production of biologically active factor X/FXa. Isolated chimeric
CC   polynucleotides are described which encode a propeptide fused to a
CC   nucleic acid sequence encoding a vitamin K-dependent protein (VKDP). The
CC   fusion proteins encoded are vitamin K-dependent protein gamma-
CC   carboxylation enhancers and are useful for optimising the gamma-
CC   carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The
CC   fusion proteins and recombinant cells expressing them are useful for
CC   alleviating a VKDP associated disease. The fusion constructs result in
CC   the production of fully gamma-carboxylated mature VKDPs, which are
CC   biologically active. The invention encompasses all combinations of
CC   propeptide sequences (modified or not) and VKDP's. This sequence encodes
CC   the signal, propeptide and mature protein sequence of human Factor IX
XX
SQ   Sequence 2775 BP; 859 A; 528 C; 564 G; 824 T; 0 U; 0 Other;

  Query Match             81.5%;  Score 1391;  DB 3;  Length 2775;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-282;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1624

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1684

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1865 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1924

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1925 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1984

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1985 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2225 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2284

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2285 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2344

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2404

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2405 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2464

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2524

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2525 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2584

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2585 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2704

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2764

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2765 TTCTGGTTCAT 2775


RESULT 6
ABV77053
ID   ABV77053 standard; DNA; 2804 BP.
XX
AC   ABV77053;
XX
DT   03-MAR-2003  (first entry)
XX
DE   Nucleotide sequence of human Factor IX.
XX
KW   Factor VIII; non-viral vesicle vector; vesicular membrane; hepatitis B;
KW   envelope protein; Factor IX; liver cell; gene therapy; haemophilia; gene;
KW   ss.
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XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             30. .1415
FT                   /*tag=  a
FT                   /product= "Factor IX"
XX
PN   WO200286091-A2.
XX
PD   31-OCT-2002.
XX
PF   25-APR-2002; 2002WO-US013164.
XX
PR   25-APR-2001; 2001US-0286314P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chien KR,  Hoshijima M;
XX
DR   WPI; 2003-093125/08.
DR   P-PSDB; ABB99529.
XX
PT   New non-viral vesicle vector comprises vesicular membrane with hepatitis
PT   B envelope protein and nucleic acid expression construct comprising
PT   complete factor VIII or IX coding sequence, useful for treating
PT   hemophilia.
XX
PS   Disclosure; Page 19-21; 34pp; English.
XX
CC   The present sequence encodes a human Factor IX. Factor IX polynucleotides
CC   are used to construct non-viral vesicle vectors. These vectors comprise a
CC   vesicular membrane with hepatitis B envelope protein exposed on the
CC   vesicle surface, and a nucleic acid expression construct comprising a
CC   complete factor VIII or factor IX coding sequence and a promoter sequence
CC   functional in liver cells. The non-viral vesicle vector is useful in gene
CC   therapy protocols for treating haemophilia
XX
SQ   Sequence 2804 BP; 868 A; 536 C; 568 G; 832 T; 0 U; 0 Other;

  Query Match             81.5%;  Score 1391;  DB 8;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-282;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2794 TTCTGGTTCAT 2804


RESULT 7
AAX28626
ID   AAX28626 standard; DNA; 2792 BP.
XX
AC   AAX28626;
```

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XX
DT   07-JUN-1999  (first entry)
XX
DE   Nucleotide sequence of human factor IX-R338A.
XX
KW   Human; Factor IX-R338A; substitution; Factor X; Factor Xa;
KW   mammalian blood coagulation cascade; phospholipid surface; calcium ion;
KW   Factor VIIIa; blood clotting; haemophilia B; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             156. .1423
FT                   /*tag=  a
FT                   /product= "Factor IX-R338A"
XX
PN   WO9903496-A1.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014750.
XX
PR   21-JUL-1997;   97US-0053571P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (STAF/) STAFFORD D W.
PA   (CHAN/) CHANG J L.
XX
PI   Stafford DW,  Chang JL;
XX
DR   WPI; 1999-131867/11.
DR   P-PSDB; AAY03203.
XX
PT   Factor IX antihemophilic factor with increased clotting activity - due to
PT   an amino aid substitution (of arginine) at position 338.
XX
PS   Disclosure; Page 26-32; 38pp; English.
XX
CC   This is the nucleotide sequence encoding a non-naturally occurring human
CC   Factor IX-R338A protein having an amino acid substitution at amino acid
CC   position 338 of arginine to alanine. Factor IX converts Factor X to
CC   Factor Xa in the mammalian blood coagulation cascade, in a process that
CC   requires a phospholipid surface, calcium ions and Factor VIIIa. Nucleic
CC   acids encoding Factor IX can be used to facilitate blood clotting, e.g.
CC   in patients afflicted with haemophilia B
XX
SQ   Sequence 2792 BP; 858 A; 541 C; 569 G; 824 T; 0 U; 0 Other;

  Query Match             81.3%;  Score 1387.8;  DB 2;  Length 2792;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-281;
  Matches 1389;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1461

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1521

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1581

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1641

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1701

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1761

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 TCTTCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1821

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1881

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1882 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1941

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2001

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2002 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2061

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2062 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2121

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2122 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2181

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2182 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2241

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2242 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2301

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2302 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2361

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2362 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2421

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2422 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2481

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       2482 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAACAGTGTTCAGAGCCAAGCAAGAAGTTGA 2541

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2542 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2601

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2602 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2661

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2662 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2721

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2722 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2781

Qy       1381 TTCTGGTTCAT 1391
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                 |||||||||||
Db        2782 TTCTGGTTCAT 2792


RESULT 8
AAN40142
ID   AAN40142 standard; cDNA; 2781 BP.
XX
AC   AAN40142;
XX
DT   25-MAR-2003  (revised)
DT   11-FEB-1992  (first entry)
XX
DE   Part of the sequence of human factor IX cDNA.
XX
KW   Christmas disease; therapy; haemophilia; factor IX; blood clotting;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     21. .143
FT                   /*tag=  a
FT   mat_peptide     144. .1391
FT                   /*tag=  b
XX
PN   WO8400560-A.
XX
PD   16-FEB-1984.
XX
PF   03-AUG-1983;   83WO-GB000191.
XX
PR   04-AUG-1982;   82GB-00022485.
PR   06-MAY-1983;   83GB-00012491.
XX
PA   (NATR ) NAT RES DEV CORP.
PA   (BROW/) BROWNLEE G G.
XX
PI   Brownlee G,  Choo KH;
XX
DR   WPI; 1984-049331/08.
DR   P-PSDB; AAP40178.
XX
PT   Recombinant DNA cloning vehicles - useful in prodn. of factor IX
PT   polypeptide and of diagnostic probes for Christmas disease.
XX
PS   Example; Fig 9; 71pp; English.
XX
CC   The inventors claim DNA molecules comprising part or all of the human
CC   factor IX DNA. The invention also includes cDNA derived from human factor
CC   IX RNA. Specifically claimed are: recombinant DNA (the phage present in
CC   clone lambda HIX-1) deposited as NCIB No. 11749; Recombinant DNA in which
CC   the cloning vehicle is the modified pAT 153 plasmid present in E.coli
CC   NCIB No. 11747; Recombinant DNA in which the bovine factor IX DNA
CC   sequence is contained in the recombinant DNA transformed into E.coli to
CC   form a clone deposited as NCIB No. 11748. (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 2781 BP; 859 A; 526 C; 567 G; 829 T; 0 U; 0 Other;

  Query Match             81.2%;  Score 1385.6;  DB 1;  Length 2781;
  Best Local Similarity   99.7%;  Pred. No. 3.6e-281;
  Matches 1388;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1449

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1509

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1569

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1629

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1689

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1749

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1809

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1869

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1929

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1989

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1990 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2049

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2050 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGGGACTTGCTTTTCAGAACATAGGGA 2109

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2169

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2229

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2289

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       2290 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTGACGAAGGCAAGATTGGCAT 2349

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2409

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2469

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2529

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2589

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
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```
Db       2590 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTTAGTTGTCCT 2649

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2709

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2769

Qy       1381 TTCTGGTTCATA 1392
              |||||||||| |
Db       2770 TTCTGGTTCAAA 2781


RESULT 9
AAT02460
ID   AAT02460 standard; mRNA; 2802 BP.
XX
AC   AAT02460;
XX
DT   15-APR-1996  (first entry)
XX
DE   Human Factor-IX mRNA.
XX
KW   Factor-IX; haemophilia; gene therapy; transgenic animal;
KW   transgenic mouse; milk; cryptic splice site; PCR; primer;
KW   polymerase chain reaction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..167
FT                   /*tag=  b
FT   CDS             30..1415
FT                   /*tag=  a
FT   mat_peptide     168..1412
FT                   /*tag=  c
FT   misc_feature    1085
FT                   /*tag=  d
FT                   /note= "base 1085 is the cryptic donor site"
FT   misc_feature    1547
FT                   /*tag=  e
FT                   /note= "base 1547 is the cryptic acceptor site"
XX
PN   WO9530000-A1.
XX
PD   09-NOV-1995.
XX
PF   02-MAY-1995;   95WO-GB000996.
XX
PR   03-MAY-1994;   94GB-00008717.
XX
PA   (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.
XX
PI   Clark AJ;
XX
DR   WPI; 1995-393074/50.
XX
PT   DNA expressing human factor IX having altered cryptic splice site - to
PT   ensure high level expression of protein in transgenic hosts, esp. in
PT   mammary glands, and for gene therapy of haemophilia.
XX
PS   Disclosure; Fig 2I-2II; 28pp; English.
XX
CC   Human Factor-IX (FIX) mRNA (AAT02460) includes cryptic donor and acceptor
CC   sites that cause a deletion of 462 nucleotides from FIX constructs
CC   expressed in transgenic animals. Improved FIX sequences have at least 1
CC   of these sites removed, so as to reduce or prevent the effects of
CC   aberrant splicing and to increase FIX yields e.g. in milk. The improved
CC   sequences may also be used in gene therapy
XX
SQ   Sequence 2802 BP; 864 A; 537 C; 571 G; 0 T; 830 U; 0 Other;
```

```
  Query Match             81.1%;  Score 1384.2;  DB 2;  Length 2802;
  Best Local Similarity   68.1%;  Pred. No. 7e-281;
  Matches  946;  Conservative  440;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||:||||||:|||:::||||||::||::||::||||::|||||::|||||||||:|:|||
Db       1414 AAUGAAAGAUGGAUUUCCAAGGUUAAUUCAUUGGAAUUGAAAAUUAACAGGGCCUCUCAC 1473

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              :|||:||:|||:::||||:|::::|::|||:::|||:|:|:|||::|:|:||:||::||:
Db       1474 UAACUAAUCACUUUCCCAUCUUUUGUUAGAUUUGAAUAUAUACAUUCUAUGAUCAUUGCU 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ::::|:|:::|||||||||||:::||:|::::|||:|| ||||::||::||||||:||||
Db       1534 UUUUCUCUUUACAGGGGAGAAUUUCAUAUUUUACCUGACCAAAUUGAUUAGAAAAUGGAA 1593

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||:|||||||:|:||:|:|::||||||::||||:||:::|:|||||||||||||::||
Db       1594 CCACUAGAGGAAUAUAAUGUGUUAGGAAAUUACAGUCAUUUCUAAGGGCCCAGCCCUUGA 1653

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              |||||::|:||||::|||::|:||||:|:|:|||:||||:||:|:||::|:||||:|:||
Db       1654 CAAAAUUGUGAAGUUAAAUUCUCCACUCUGUCCAUCAGAUACUAUGGUUCUCCACUAUGG 1713

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||:|||:|||:|||::::|||:||::|||||||::|||:|::|||||:|::|:::||:
Db       1714 CAACUAACUCACUCAAUUUUCCCUCCUUAGCAGCAUUCCAUCUUCCCGAUCUUCUUUGCU 1773

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              :|:||||||||||||:|||:|:::|::||::|:|:|:||||:||||||:|:::||:|:||
Db       1774 UCUCCAACCAAAACAUCAAUGUUUAUUAGUUCUGUAUACAGUACAGGAUCUUUGGUCUAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              :|:|:|||||||||||:|||||||:||:||||||||||||||||||:|||:|||||||:|
Db       1834 UCUAUCACAAGGCCAGUACCACACUCAUGAAGAAAGAACACAGGAGUAGCUGAGAGGCUA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||:||:|||||||||:||:||::::||:|:||||:|::||:|||:|::::|||::::|
Db       1894 AAACUCAUCAAAAACACUACUCCUUUUCCUCUACCCUAUUCCUCAAUCUUUUACCUUUUC 1953

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||:|||||:|||||||:|||:::::|:|:::|::||:|||:|:|:|||::::||||:|
Db       1954 CAAAUCCCAAUCCCCAAAUCAGUUUUUCUCUUUCUUACUCCCUCUCUCCCUUUUACCCUC 2013

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||:||:||::||||||||||:||||||||:||::|:|::|:||::|:|:||||||::|:|
Db       2014 CAUGGUCGUUAAAGGAGAGAUGGGGAGCAUCAUUCUGUUAUACUUCUGUACACAGUUAUA 2073

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||:|:|:|:|||||||||||::||::|||:||:|| |||::||::::|||||||:|||||
Db       2074 CAUGUCUAUCAAACCCAGACUUGCUUCCAUAGUGGGGACUUGCUUUUCAGAACAUAGGGA 2133

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              :||||:||||:|||:||||||:::||||||||||:::|:::|||||||::|||::|::::
Db       2134 UGAAGUAAGGUGCCUGAAAAGUUUGGGGGAAAAGUUUCUUUCAGAGAGUUAAGUUAUUUU 2193

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              |:|:|:|:||:|:|:|:|:||||:|:|:||:|:||||:|:|||:|:|:||:|:|:|:|:|
Db       2194 AUAUAUAUAAUAUAUAUAUAAAAUAUAUAAUAUACAAUAUAAAUAUAUAGUGUGUGUGUG 2253

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              :|:|||:|:|:|:|||||||||||||:|||||||:|:||:||||||||:||||||::|:|
Db       2254 UAUGCGUGUGUGUAGACACACACGCAUACACACAUAUAAUGGAAGCAAUAAGCCAUUCUA 2313

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              |||||::|:|:||::|:|||||:|:|||:|||||:||::: ||||||||||||::||||:
Db       2314 AGAGCUUGUAUGGUUAUGGAGGUCUGACUAGGCAUGAUUUGACGAAGGCAAGAUUGGCAU 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              |:||::|:|||:||||||||:||||::||||||||||:|::|:||:|:::|:|||||:||
Db       2374 AUCAUUGUAACUAAAAAAGCUGACAUUGACCCAGACAUAUUGUACUCUUUCUAAAAAUAA 2433
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Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              :||:||:||:||:|||||||||||||||||||::||:::||||:|:|||||:||:|||||
Db       2434 UAAUAAUAAUGCUAACAGAAAGAAGAGAACCGUUCGUUUGCAAUCUACAGCUAGUAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              |:::|||||||||::|||||||:|:|:|::||||||:|::||||||||||||||||::||
Db       2494 CUUUGAGGAAGAAUUCAACAGUGUGUCUUCAGCAGUGUUCAGAGCCAAGCAAGAAGUUGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||::|||:||||||||||||||:|||:|:||:|:|:||:::|||:||||:||||||||:|
Db       2554 AGUUGCCUAGACCAGAGGACAUAAGUAUCAUGUCUCCUUUAACUAGCAUACCCCGAAGUG 2613

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||:|||||||||:||||||||:|||:||::||||:||||||||:|||::|:||:
Db       2614 GAGAAGGGUGCAGCAGGCUCAAAGGCAUAAGUCAUUCCAAUCAGCCAACUAAGUUGUCCU 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              :::|:||:::||:|::|||||:||||||::::||::|:||::||:||::|:|:|::|||:
Db       2674 UUUCUGGUUUCGUGUUCACCAUGGAACAUUUUGAUUAUAGUUAAUCCUUCUAUCUUGAAU 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              |::|:|||||||::||:|||||||:||||:|:|:::|||:::|:|||::||:||||:||:|
Db       2734 CUUCUAGAGAGUUGCUGACCAACUGACGUAUGUUUCCCUUUGUGAAUUAAUAAACUGGUG 2793

Qy       1381 TTCTGGTTC 1389
              ::|:||::|
Db       2794 UUCUGGUUC 2802

RESULT 10
AAN40177
ID   AAN40177 standard; cDNA; 2781 BP.
XX
AC   AAN40177;
XX
DT   25-MAR-2003  (revised)
DT   13-FEB-1992  (first entry)
XX
DE   Part of the sequence of human factor IX cDNA.
XX
KW   Haemophilia; Christmas disease; diagnosis; treatment; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     21. .143
FT                   /*tag=  a
FT   exon            94. .257
FT                   /*tag=  c
FT                   /label= t
FT   mat_peptide     144. .1391
FT                   /*tag=  b
FT   exon            258. .292
FT                   /*tag=  d
FT                   /label= u
FT   exon            293. .396
FT                   /*tag=  e
FT                   /label= v
FT   exon            397. .525
FT                   /*tag=  f
FT                   /label= w
FT   exon            526. .728
FT                   /*tag=  g
FT                   /label= x
FT   exon            729. .843
FT                   /*tag=  h
FT                   /label= y
FT   exon            844. .2781
FT                   /*tag=  i
FT                   /label= z
XX
PN   GB2125409-A.
XX
```

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PD   07-MAR-1984.
XX
PF   03-AUG-1983;   83GB-00020975.
XX
PR   04-AUG-1982;   82GB-00022486.
PR   16-MAY-1983;   83GB-00012490.
XX
PA   (NATR ) NAT RES DEV CORP.
XX
PI   Brownlee GG,  Choo KH;
XX
DR   WPI; 1984-057898/10.
DR   P-PSDB; AAP40222.
XX
PT   Prodn. of artificial human factor IX - by use of recombinant DNA
PT   sequences for host transformation and cultivation.
XX
PS   Example; Fig 9; 49pp; English.
XX
CC   The inventors claim a recombinant DNA having a human factor IX sequence
CC   pref. at least 50 nucleotides long, esp. 75-27000 nucleotides. A cloning
CC   vector contg. foreign DNA is also claimed. The foreign sequence pref.
CC   includes the whole of an exon sequence of the human factor IX genome. The
CC   cloning vehicle may be a modified pAT 153 plasmid. Also claimed is a
CC   labelled diagnostic probe comprising a DNA molecule having a single- or
CC   double-stranded probe sequence of 15 to 10000 nucleotides long Factor IX
CC   DNA sequence. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 2781 BP; 861 A; 531 C; 563 G; 826 T; 0 U; 0 Other;

  Query Match             80.8%;  Score 1379.2;  DB 1;  Length 2781;
  Best Local Similarity   99.4%;  Pred. No. 7.9e-280;
  Matches 1384;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1449

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1509

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1569

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1629

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1689

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1749

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1809

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TCTATCACAACGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1869

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1929

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1989
```

```
Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1990 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTAATA 2049

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2050 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGGGACTTGCTTTTCAGAACATAGGGA 2109

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2110 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTATAGTTATTTT 2169

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2229

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2289

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       2290 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTGACGAAGGCAAGATTGGCAT 2349

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2409

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       2410 TAATAATAATGCTAACAGAAAGAAGACAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2469

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2529

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2589

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2649

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2709

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2769

Qy       1381 TTCTGGTTCATA 1392
              |||||||||| |
Db       2770 TTCTGGTTCAAA 2781


RESULT 11
ADQ38340
ID   ADQ38340 standard; DNA; 2728 BP.
XX
AC   ADQ38340;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 3.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
DR   P-PSDB; ADQ39168.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a human myocardial infarction-
CC   associated gene containing one or more SNP's of the invention. Note: This
CC   sequence was not shown in the specification. The sequence has come from
CC   an electronic sequence listing downloaded from the WIPO website.
XX
SQ   Sequence 2728 BP; 798 A; 468 C; 450 G; 730 T; 0 U; 282 Other;

  Query Match             80.6%;  Score 1376.6;  DB 13;  Length 2728;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-279;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1340 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1399

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1400 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1459

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1460 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1519

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1520 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1579
```

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Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1580 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1639

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1699

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1759

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1760 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1819

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1820 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1879

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1939

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1940 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 1999

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2000 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2059

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2060 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2119

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2120 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2177

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2178 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2237

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2238 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2297

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2298 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2357

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2358 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2417

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2418 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2477

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2478 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2537

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2538 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2597

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2598 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2657
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Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2658 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2717

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2718 TTCTGGTTCAT 2728


RESULT 12
ADQ38338
ID   ADQ38338 standard; DNA; 2771 BP.
XX
AC   ADQ38338;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 1.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
DR   P-PSDB; ADQ39166.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 1; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a human myocardial infarction-
CC   associated gene containing one or more SNP's of the invention. Note: This
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CC   sequence was not shown in the specification. The sequence has come from
CC   an electronic sequence listing downloaded from the WIPO website.
XX
SQ   Sequence 2771 BP; 804 A; 485 C; 456 G; 753 T; 0 U; 273 Other;

  Query Match             80.6%;  Score 1376.6;  DB 13;  Length 2771;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-279;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1442

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1502

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1562

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1622

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1682

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1742

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1802

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1862

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1922

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1982

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2042

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2043 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2102

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2162

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2163 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2220

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2280

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2340

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2400

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2460

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2520

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2580

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2640

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2700

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2760

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2761 TTCTGGTTCAT 2771


RESULT 13
ADQ38339
ID   ADQ38339 standard; DNA; 2777 BP.
XX
AC   ADQ38339;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 2.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
DR   P-PSDB; ADQ39167.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 2; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
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CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a human myocardial infarction-
CC   associated gene containing one or more SNP's of the invention. Note: This
CC   sequence was not shown in the specification. The sequence has come from
CC   an electronic sequence listing downloaded from the WIPO website.
XX
SQ   Sequence 2777 BP; 801 A; 489 C; 452 G; 754 T; 0 U; 281 Other;

  Query Match             80.6%;  Score 1376.6;  DB 13;  Length 2777;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-279;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1389 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1448

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1449 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1508

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1509 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1568

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1569 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1628

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1629 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1688

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1689 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1748

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1749 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1808

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1809 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1868

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1869 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1928

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1929 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1988

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1989 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2048

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        2049 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2108

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2109 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2168

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATATAGTGTGTGTG 840
               |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        2169 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2226

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2227 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2286

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2287 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2346

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2347 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2406

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2407 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2466

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2467 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2526

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2527 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2586

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2587 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2646

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2647 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2706

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2707 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2766

Qy        1381 TTCTGGTTCAT 1391
               |||||||||||
Db        2767 TTCTGGTTCAT 2777


RESULT 14
ADQ38341
ID   ADQ38341 standard; DNA; 2831 BP.
XX
AC   ADQ38341;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 4.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
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XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
DR   P-PSDB; ADQ39169.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 4; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a human myocardial infarction-
CC   associated gene containing one or more SNP's of the invention. Note: This
CC   sequence was not shown in the specification. The sequence has come from
CC   an electronic sequence listing downloaded from the WIPO website.
XX
SQ   Sequence 2831 BP; 821 A; 494 C; 465 G; 764 T; 0 U; 287 Other;

  Query Match             80.6%;  Score 1376.6;  DB 13;  Length 2831;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-279;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1502

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1562

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1622

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1682

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1742

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1802

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1862

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1922

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1982

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2042

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2102

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2103 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2162

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2163 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2222

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2223 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2280

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2340

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2400

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2460

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2520

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2580

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2640

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2700

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2760

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2820

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2821 TTCTGGTTCAT 2831


RESULT 15
ACN43105
ID   ACN43105 standard; cDNA; 2758 BP.
XX
AC   ACN43105;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1980.
XX
KW   ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW   dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   P-PSDB; ABM84453.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 1; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp polynucleotide of
CC   the invention. Note: The sequence data for this patent is not represented
CC   in the printed specification, but was obtained in electronic format
CC   directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 2758 BP; 858 A; 537 C; 548 G; 815 T; 0 U; 0 Other;

  Query Match             80.5%;  Score 1373.4;  DB 13;  Length 2758;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-278;
  Matches 1386;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1431

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1491

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1551

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1611

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1612 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1671

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1672 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1731

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1732 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1791

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1792 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1851

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1852 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1911

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1912 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1971

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1972 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2031

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       2032 CATGTCTATCAAACCCAGACTTGCTTCCGTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2091

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2092 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2151

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2152 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2209

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2210 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2269

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2270 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2329

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2330 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2389

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2390 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2449

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2450 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2509

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db        2570 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2629

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2630 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2689

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2690 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2749

Qy        1381 TTCTGGTTC 1389
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Db        2750 TTCTGGTTC 2758

Search completed: April 18, 2006, 13:22:09
Job time : 1040.57 secs
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                   GenCore version 5.1.7
          Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:18:29 ; Search time 8289.18 Seconds
                                           (without alignments)
                                           9634.919 Million cell updates/sec

Title:          US-09-884-901A-7
Perfect score:  1707
Sequence:       1 aatgaaagatggatttccaa..........ggagtttcaggccaagctta 1707

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:      82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                1:  gb_est1:*
                2:  gb_est2:*
                3:  gb_est3:*
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                6:  gb_est5:*
                7:  gb_est6:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                   %
Result             Query
  No.    Score     Match Length DB  ID                     Description
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c  1       802     47.0    943  5  BX405727               BX405727 BX405727
   2     527.2     30.9    532  6  CB156936               CB156936 K-EST0215
c  3     486.6     28.5    515  5  BX414387               BX414387 BX414387
   4     451.2     26.4    524  7  CO775183               CO775183 ILLUMIGEN
   5       446     26.1    518  9  AQ456663               AQ456663 HS_5166_A
   6       373     21.9    373  1  AV647038               AV647038 AV647038
   7       373     21.9    374  1  AV647182               AV647182 AV647182
   8       321     18.8    385  1  AV656454               AV656454 AV656454
c  9     236.8     13.9    721  1  AM018125               AM018125 AM018125
  10     163.6      9.6    583  7  CO740602               CO740602 SlLL07a27
  11     149.6      8.8    374  6  CF106639               CF106639 ZP0904D3
  12     149.6      8.8    688  5  BX926315               BX926315 BX926315
  13     149.6      8.8    690  5  BX925779               BX925779 BX925779
  14       147      8.6    257  7  CO775581               CO775581 ILLUMIGEN
c 15     142.4      8.3    400  7  CO701325               CO701325 DG32-1f6
  16     138.2      8.1    731  1  AM018944               AM018944 AM018944
c 17     122.4      7.2    592  10  CE730574               CE730574 tigr-gss-
  18     119.6      7.0    744  1  AM019095               AM019095 AM019095
  19     118.6      6.9    835  1  AM015797               AM015797 AM015797
  20     118.2      6.9    816  6  CA456053               CA456053 AGENCOURT
c 21     113.8      6.7    799  1  AM014733               AM014733 AM014733
c 22     107.4      6.3    574  3  BP104057               BP104057 BP104057
  23      91.8      5.4    533  7  CN438614               CN438614 BE04016A2
c 24      91.6      5.4    583  3  BP103684               BP103684 BP103684
  25      86.6      5.1    525  5  BX514685               BX514685 BX514685
c 26      86.2      5.0    363  5  BU182460               BU182460 AGENCOURT
  27      86.2      5.0    698  9  AQ741865               AQ741865 HS_5568_B
c 28      84.4      4.9    681  10  AG115419               AG115419 Pan trogl
  29      84.2      4.9    647  10  AG017260               AG017260 Homo sapi
  30        84      4.9    233  9  AQ426652               AQ426652 CITBI-E1-
c 31      83.8      4.9    464  3  BP101424               BP101424 BP101424
c 32      83.4      4.9    310  1  AL603386               AL603386 DKFZp686D
c 33      83.4      4.9    366  1  AL603402               AL603402 DKFZp686E
  34      83.4      4.9    763  9  BZ610396               BZ610396 WHAAX81TR
c 35      83.2      4.9    511  9  BZ612790               BZ612790 WHAAS15TF
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c 38      82.6      4.8    310  1  AW407679               AW407679 UI-HF-BM0
  39      82.6      4.8    396  1  AA569240               AA569240 nm31b04.s
  40      82.4      4.8    528  9  AQ211789               AQ211789 HS_3234_B
c 41      81.8      4.8    389  3  BP102450               BP102450 BP102450
c 42      81.6      4.8    477  8  DR033758               DR033758 5000DCE12
  43      81.2      4.8    409  9  B55158                 B55158 CIT-HSP-386
  44      81.2      4.8    602  9  AQ488141               AQ488141 RPCI-11-2
c 45      81.2      4.8    840  8  CX871715               CX871715 HESC4_60_


                                ALIGNMENTS


RESULT 1
BX405727/c
LOCUS       BX405727                 943 bp    mRNA    linear   EST 01-MAY-2004
DEFINITION  BX405727 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM008YI08 3-PRIME, mRNA sequence.
ACCESSION   BX405727
VERSION     BX405727.2  GI:46924492
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 943)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30635411.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 10715.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0AM008BE04NP1&c=10715.f.
FEATURES             Location/Qualifiers
     source          1. .943
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                     /mol_type="mRNA"
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                     /clone="CS0DM008YI08"
                     /tissue_type="FETAL LIVER"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL LIVER"
                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
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  Query Match             47.0%;  Score 802;  DB 5;  Length 943;
  Best Local Similarity   89.2%;  Pred. No. 9.7e-164;
  Matches  847;  Conservative   47;  Mismatches   48;  Indels    8;  Gaps    4;

Qy        412 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCT 471
              |||||| |    |||||||| ||||::|:| ||||||: :||| || ||| |: ::||||
Db        943 TTGGTCCAAAAAATCACAAGCCCAGKMCYARACTCATSTRGAAGGATCACCGSGKKAGCT 884

Qy        472 GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT 531
              |:| ::|||||| || |: ||||||:|||||| ||| ||||::|||||| | :|||||||
Db        883 GMGYKSCTAAAATTCTTY-AAAACAMTACTCC-TTTACTCTMMCCTATTACAMAATCTTT 826

Qy        532 TACCTTTTCCAAATCCCAATCCCC-AAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
               ||| |||| ||||:|:||||||| |||||||||||||||||||||||||||| ||||||
Db        825 NACCATTTCAAAATMCMAATCCCCMAAATCAGTTTTTCTCTTTCTTACTCCCTATCTCCC 766

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              |||||||||||||::||:||||||||||||||||::|||||:|  |:||||||||:|| |
Db        765 TTTTACCCTCCATSRTCRTTAAAGGAGAGATGGGKMGCATCWTCATSTTATACTTMTGAA 706

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              |||||:|||||||||||||:||||||| ||| :||::| ||:|||| |:||||||:::||
Db        705 CACAGWTATACATGTCTATMAAACCCAAACTCKCTWMCTTADTGGAAAHTTGCTTWWMAG 646

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||:|||||||||||:|||||| ||| |||:|:|::|
Db        645 AACATAGGGATGAAGTAAGGTGCCTGWAAAGTTTGGGGSAAAAGTCTCTCTCASASASWT 586

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              |||:||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AAGWTATTTTWTATATATAATATATATATAAAATATATAATATACAATATAAATATATA- 527.

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
                   |  :|| |  ||||||||| |||||||||||||||||||||||||||||||||||
Db        526 ----NGNTKGTTTATGTGTGTGTAAACACACACGCATACACACATATAATGGAAGCAATA 471

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
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Db        470 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 411

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              |||||||||||||||||||||||||||||||:|||||||||||:||||||||||||||||
Db        410 AGATTGGCATATCATTGTAACTAAAAAAGCTSACATTGACCCABACATATTGTACTCTTT 351

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 291

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 231

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        230 AAGAAGTTGAAGTTGCCTAGACCAGAGTACATAAGTATCATGTCTCCTTTAACTAGCATA 171

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
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Db        170 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 111

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
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Db        110 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 51

Qy       1311 TATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTT 1360
              |||||||||||||||||||||| | |||||   | |||||| || || ||
Db         50 TATCTTGAATCTTCTAGAGAGTNGNTGACCNNATNACGTATTTTCCCTTT 1


RESULT 2
CB156936
LOCUS       CB156936                 532 bp    mRNA    linear   EST 29-JAN-2003
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DEFINITION  K-EST0215940 L17N670205n1 Homo sapiens cDNA clone
            L17N670205n1-6-A08 5', mRNA sequence.
ACCESSION   CB156936
VERSION     CB156936.1  GI:28142066
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 532)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project.2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 6  row: A  column: 08
            High quality sequence stop: 532.
FEATURES             Location/Qualifiers
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                     /clone="L17N670205n1-6-A08"
                     /sex="F"
                     /lab_host="Top10F'"
                     /clone_lib="L17N670205n1"
                     /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

  Query Match             30.9%;  Score 527.2;  DB 6;  Length 532;
  Best Local Similarity   99.4%;  Pred. No. 6e-104;
  Matches  529;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        205 GGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGACAAAATTGTGAAGTTAAATTCTCC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGACAAAATTGTGAAGTTAAATTCTCC 120

Qy        265 ACTCTGTCCATCAGATACTATGGTTCTCCACTATGGCAACTAACTCACTCAATTTTCCCT 324
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Db        121 ACTCTGTCCATCAGATACTATGGTTCTCCACTATGGCAACTAACTCACTCAATTTTCCCT 180

Qy        325 CCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCTTCTCCAACCAAAACATCAATGTTT 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCTTCTCCAACCAAAACATCAATGTTT 240

Qy        385 ATTAGTTCTGTATACAGTACAGGATCTTTGGTCTACTCTATCACAAGGCCAGTACCACAC 444
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Db        241 ATTAGTTCTGTATACAGTACAGGATCTTTGGTCTACTCTATCACAAGGCCAGTACCACAC 300

Qy        445 TCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTAAAACTCATCAAAAACACTACTCCT 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        505 TTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTCCAAATCCCAATCCCCAAATCAGTT 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTCCAAATCCCAATCCCCAAATCAGTT 420
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Qy        565 TTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTCCATGGTCGTTAAAGGAGAGATGGG 624
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Db        421 TTTTTTTTTTTTACTCCCTCTCTCCCTTTTACCCTCCATGGTCGTTAAAGGAGAGATGGG 480

Qy        625 GAGCATCATTCTGTTATACTTCTGTACACAGTTATACATGTCTATCAAACCC 676
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Db        481 GAGCATCATTCTGTTATACTTCTGTACACAGTTATACATGTCTATCAAACCC 532


RESULT 3
BX414387/c
LOCUS       BX414387                 515 bp    mRNA    linear   EST 01-MAY-2004
DEFINITION  BX414387 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM008YI08 3-PRIME, mRNA sequence.
ACCESSION   BX414387
VERSION     BX414387.2  GI:46928493
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30645720.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 10715.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAK078AH02NM1&c=10715.f.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DM008YI08"
                     /tissue_type="FETAL LIVER"
                     /dev_stage="fetal"
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                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             28.5%;  Score 486.6;  DB 5;  Length 515;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-95;
  Matches  489;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Db        515 TNCACACATATAATGGAAGCAATAAGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTG 456

Qy        927 ACTAGGCATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAGCTGACAT 986
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Db        455 ACTAGGCATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAGCTGACAT 396

Qy        987 TGACCCAGACATATTGTACTCTTTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGA 1046
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Db        395 TGACCCAGACATATTGTACTCTTTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGA 336

Qy       1047 GAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGT 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 GAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGT 276

Qy       1107 CTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGT 1166
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Db        275 CTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGT 216

Qy       1167 ATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGC 1226
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Qy       1287 CATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGA 1346
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Db         95 CATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGA 36

Qy       1347 CGTATGTTTCCCTT 1360
              ||||  ||  || ||
Db         35 CGTAGTTTCCCTTT 22


RESULT 4
CO775183
LOCUS       CO775183                 524 bp    mRNA    linear   EST 04-AUG-2004
DEFINITION  ILLUMIGEN_MCQ_52421 Katze_MNLV Macaca nemestrina cDNA clone
            IBIUW:28458 5' similar to Bases 5 to 424 highly similar to human F9
            (Hs.1330), mRNA sequence.
ACCESSION   CO775183
VERSION     CO775183.1  GI:50976446
KEYWORDS    EST.
SOURCE      Macaca nemestrina (pig-tailed macaque)
  ORGANISM  Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 524)
  AUTHORS   Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
            Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
            Iadonato,S.P.
  TITLE     Analysis of the Macaca mulatta transcriptome and the sequence
            divergence between Macaca and human
  JOURNAL   Genome Biol. 6 (7), R60 (2005)
   PUBMED   15998449
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.21. 661 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 524   Std Error: 0.00
            Plate: CL000532  row: F  column: 07
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .524
                     /organism="Macaca nemestrina"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9545"
                     /clone="IBIUW:28458"
                     /sex="male"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MNLV"
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                     /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN

  Query Match             26.4%;  Score 451.2;  DB 7;  Length 524;
  Best Local Similarity   94.2%;  Pred. No. 2.1e-87;
  Matches  490;  Conservative    0;  Mismatches   28;  Indels    2;  Gaps    2;

Qy        974 AAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAA-TAATAATAATAATGC 1032
              ||||||||||||||||| |||| ||||||||||||||||||||| |||||||||||||||
Db          5 AAAAAGCTGACATTGACGCAGATATATTGTACTCTTTCTAAAAATTAATAATAATAATGC 64

Qy       1033 TAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGA 1092
              |||||||||||||||||| | || |||||| |||||| ||||||||||||||||||||||
Db         65 TAACAGAAAGAAGAGAACAGCTCATTTGCAGTCTACAACTAGTAGAGACTTTGAGGAAGA 124

Qy       1093 ATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGAC 1152
              ||||||||| |||||||||||||||||||||| |||| ||||||||||||||||||||||
Db        125 ATTCAACAGCGTGTCTTCAGCAGTGTTCAGAGTCAAGAAAGAAGTTGAAGTTGCCTAGAC 184

Qy       1153 CAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCC-GAAGTGGAGAAGGGTGC 1211
              ||||||||||||||| |||||||||||||||| |||| |||| |||||||||||||||||
Db        185 CAGAGGACATAAGTAACATGTCTCCTTTAACTGGCATGCCCCTGAAGTGGAGAAGGGTGC 244

Qy       1212 AGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTC 1271
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGCAGGCTCGAAGACATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTC 304

Qy       1272 GTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAG 1331
               |||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        305 ATGTTCACCGTGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATTTTCTAGAGAG 364

Qy       1332 TTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTGTTCTGGTTCAT 1391
              |||||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||
Db        365 TTGCTGACCAACAGACGTATGTTTCCCTTCGTGAATTAATAAACTGGTGTTCTGGTTCAT 424

Qy       1392 ACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATTTGATGATGCAT 1451
              |||||||||||||||| || |||||||||||| |||| ||||||||||||||||||||||
Db        425 ACCTTGGCTTTTTGTGAATCCCATTGATGTGATTCAGCCACCCTGTATTTGATGATGCAT 484

Qy       1452 GGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCT 1491
               ||||||||||||||||||||  ||||| |||||||||||
Db        485 AGGACTACTGACAAAATCACTTCGACCCCGCCAAGCTGCT 524


RESULT 5
AQ456663
LOCUS       AQ456663                 518 bp    DNA     linear   GSS 21-APR-1999
DEFINITION  HS_5166_A1_C10_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=742 Col=19 Row=E, genomic survey sequence.
ACCESSION   AQ456663
VERSION     AQ456663.1  GI:4591998
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 742  row: E  column: 19
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 518.
FEATURES             Location/Qualifiers
     source          1..518
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=742 Col=19 Row=E"
                     /sex="male"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match             26.1%;  Score 446;  DB 9;  Length 518;
  Best Local Similarity   94.6%;  Pred. No. 2.8e-86;
  Matches  458;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1091 GAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAG 1150
              | |     ||| | | ||||||||||||||| ||||||||||||||||||||||| ||||
Db         35 GTANNNCCCAGCGNGNCTTCAGCAGTGTTCACAGCCAAGCAAGAAGTTGAAGTTGTCTAG 94

Qy       1151 ACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTG 1210
              |||||| |||||   |||||||||||||||||||||||||||||||||||||||| ||||
Db         95 ACCAGATGACATTTTTATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAAGGTG 154

Qy       1211 CAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTT 1270
              || || |||||||||||||| ||||||||||||||||||||| |||||||||||||||||
Db        155 CATCACGCTCAAAGGCATAAATCATTCCAATCAGCCAACTAAATTGTCCTTTTCTGGTTT 214

Qy       1271 CGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGA 1330
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        215 CGTGTTCACCATGGAACATTTTGATTATAGNTAATCCTTCTATCTTGAATCTTCTAGAGA 274

Qy       1331 GTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTGTTCTGGTTCA 1390
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        275 GTTGCTGACCAACTGACGTATGTTTCCCTCTGTGAATTAATAAACTGGTGTTCTGGTTCA 334

Qy       1391 TACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATTTGATGATGCA 1450
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        335 TACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCACTCACCCTGTATTTGATGATGCA 394

Qy       1451 TGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCCTGCCCCAACC 1510
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        395 TGGGACTACTGACAAAATCACTCTGACCCCGCCAAGCTGCTGCCTTCTCCTGCCCCAACC 454

Qy       1511 TCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTCAATATATTTT 1570
              ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        455 TCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAAGTCTTTTAGTCAATATATTTT 514

Qy       1571 TGTC 1574
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Db        515 TGTC 518


RESULT 6
AV647038
LOCUS       AV647038                 373 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AV647038 GLC Homo sapiens cDNA clone GLCAUA09 3', mRNA sequence.
ACCESSION   AV647038
VERSION     AV647038.1  GI:9868052
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1..373
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCAUA09"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             21.9%;  Score 373;  DB 1;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-70;
  Matches  373;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 GCTTTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATG 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTTTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATG 60

Qy        178 GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT 120

Qy        238 TGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTA 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTA 180

Qy        298 TGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTT 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTT 240

Qy        358 GCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 300

Qy        418 TACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGG 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGG 360

Qy        478 CTAAAACTCATCA 490
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Db        361 CTAAAACTCATCA 373


RESULT 7
AV647182
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LOCUS       AV647182                 374 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AV647182 GLC Homo sapiens cDNA clone GLCAVF01 3', mRNA sequence.
ACCESSION   AV647182
VERSION     AV647182.1  GI:9868196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1..374
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCAVF01"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             21.9%;  Score 373;  DB 1;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-70;
  Matches  373;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 GCTTTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATG 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTTTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATG 60

Qy        178 GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT 237
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Db         61 GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT 120

Qy        238 TGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTA 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTA 180

Qy        298 TGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTT 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTT 240

Qy        358 GCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 300

Qy        418 TACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGG 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGG 360

Qy        478 CTAAAACTCATCA 490
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Db        361 CTAAAACTCATCA 373
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```
RESULT 8
AV656454
LOCUS       AV656454                 385 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV656454 GLC Homo sapiens cDNA clone GLCERE05 3', mRNA sequence.
ACCESSION   AV656454
VERSION     AV656454.1  GI:9877468
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 385)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .385
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCERE05"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             18.8%;  Score 321;  DB 1;  Length 385;
  Best Local Similarity   87.7%;  Pred. No. 4.5e-59;
  Matches  385;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

Qy         933 CATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCC 992
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Db           1 CATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCC 60

Qy         993 AGACATATTGTACTCTTTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCG 1052
               |||||||||||||||||
Db          61 AGACATATTGTACTCTT------------------------------------------- 77

Qy        1053 TTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAG 1112
                          |||||||||||||||||||||||||||||||||||||||||||||||||
Db          78 -----------TCTACAGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAG 126

Qy        1113 CAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATG 1172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         127 CAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATG 186

Qy        1173 TCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGT 1232
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         187 TCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGT 246

Qy        1233 CATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTT 1292
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         247 CATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTT 306
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Qy        1293 GATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGACGTATG 1352
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         307 GATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGACGTATG 366

Qy        1353 TTTCCCTTTGTGAATTAAT 1371
               |||||||||||||||||||
Db         367 TTTCCCTTTGTGAATTAAT 385


RESULT 9
AM018125/c
LOCUS       AM018125                 721 bp    mRNA    linear   EST 29-JUN-2005
DEFINITION  AM018125 KN-252-liver, Bos taurus Bos taurus cDNA clone C0007416a18
            3', mRNA sequence.
ACCESSION   AM018125
VERSION     AM018125.1  GI:68319317
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Anderson,S.I., Taylor,R., Talbot,R., Speed,D., Law,A.S.,
            Humphray,S., Hanotte,O., Mwakaya,J. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying host responses
            to trypanosome infection in cattle
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="C0007416a18"
                     /tissue_type="liver"
                     /clone_lib="KN-252-liver, Bos taurus"
                     /note="breed: N'dama"
ORIGIN

  Query Match             13.9%;  Score 236.8;  DB 1;  Length 721;
  Best Local Similarity   67.9%;  Pred. No. 9.6e-41;
  Matches  429;  Conservative    0;  Mismatches  177;  Indels   26;  Gaps    6;

Qy           1 AATGAAAGATGGATTTCCAAGG-TTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCA 59
               || |||| ||| |||||||||| | |  |  ||||||||||| ||  ||| || |  | |
Db         629 AAAGAAAAATGTATTTCCAAGGCTGACATATTTGGAATTGAACATGGACAAGGTCCTTTA 570

Qy          60 CTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGC 119
               |||| ||||||||||||||| | |  ||||||||||   ||||| ||||| ||  ||| |
Db         569 CTAAATAATCACTTTCCCATTTCT--TTAGATTTGAGGGTATACCTTCTAAGAAAATTCC 512

Qy         120 TTTTTCTCTTTACAGGGGAGA----------ATTTCATATTTTACCTGAGCAAATTGATT 169
               ||||| | ||||  |||   |          | ||||| |||| |  ||  || | |||
Db         511 TTTTTTTTTTTATGGGGAGAAGTTTAGCTAGACTTCATTTTTTTCTAGAATAAGTAGATA 452

Qy         170 AGAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGC 229
               |||||||| || | |||||| || ||| ||||   |||||||   | |||| ||   ||
Db         451 AGAAAATGTAATCCCTAGAGAAACATACTGTGGGGGGAAATTGTGGCCATTCCTTCAGGT 392

Qy         230 CCAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTT 289
               |||||||||||| |||||| |||||||| || | ||  ||| |||||||  | | | |||
Db         391 CCAGCCCTTGACCAAATTGGGAAGTTAAGTTTTTCATCCTGCCCATCAGGCATTGTAGTT 332

Qy         290 CTCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGA 349
                ||||     |||||| |||       ||||   |||||||||||||||||  | || ||
Db         331 TTCCAGGGGAGCAACTCACT-----GTTTTTTTGTCCTTAGCAGCATTCCACATGCCAGA 277

Qy         350 TCTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGAT 409
```

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              | || ||  | || ||  || ||     ||| | |   | || |        | ||||||
Db        276 TTTTTTTAACATCCCCCCCCCAAGTTAAAATTTATTGGATTTGT-------ATCCAGGAT 224

Qy        410 CTTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAG 469
                ||||| || || |||| ||||||||  ||||| ||||  || ||||||||||||| ||
Db        223 ACTTGGTTTAGTCCATCATAAGGCCAGCCCCACATTCATTCAGGAAGAACACAGGAGCAG 164

Qy        470 CTGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTA-CCCTATTCCTCAATC 528
               ||||||  ||||| ||||   ||||||||||  |||| |  || || |||||||  |||
Db        163 GTGAGAGATTAAAAGTCATGGGAAACACTACTTTTTTTTCAATATCCTTATTCCTGCATC 104

Qy        529 TTTTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTC 588
               |||| | ||||||  ||| ||| ||||||||| ||||| | ||| || | || | || |
Db        103 CTTTATCCTTTCCACCTCCTAATGCCCAAATCACTTTTTTTTTTTTTTTCCCCTTTTCCC 44

Qy        589 CCTTTTACCCTCCATGGTCGTTAAAGGAGAGA 620
                  |   | |  | ||  |  || | | | |
Db         43 TACATAGGCATTAAAGGGGGGAAAGGAAAAAA 12


RESULT 10
CO740602
LOCUS       CO740602                 583 bp    mRNA    linear   EST 29-JUL-2004
DEFINITION  S1LL07a27j01f1 squirrel liver library 3 Spermophilus lateralis cDNA
            clone 27j01 5', mRNA sequence.
ACCESSION   CO740602
VERSION     CO740602.1  GI:50827872
KEYWORDS    EST.
SOURCE      Spermophilus lateralis (golden-mantled ground squirrel)
  ORGANISM  Spermophilus lateralis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
REFERENCE   1  (bases 1 to 583)
  AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
            Rogers,J. and Cossins,A.R.
  TITLE     Microarray analysis of transcriptional changes during hibernation
            in the golden mantled ground squirrel, Spermophilus lateralis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 27  row: j  column: 01
            Seq primer: TriplEx 5'LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3')
            High quality sequence stop: 583.
FEATURES             Location/Qualifiers
     source          1..583
                     /organism="Spermophilus lateralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:76772"
                     /clone="27j01"
                     /sex="Male & female"
                     /tissue_type="liver"
                     /dev_stage="Adult"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel liver library 3"
                     /note="Vector: pTriplEx2; Site_1: Sfi1 GGCCATTACGGCC;
                     Site_2: Sfi1 GGCCGCCTCGGCC; Normalized cDNA library
                     prepared from liver of hibernating and summer animals"
ORIGIN

  Query Match             9.6%;  Score 163.6;  DB 7;  Length 583;
  Best Local Similarity   67.9%;  Pred. No. 8.1e-25;
  Matches  326;  Conservative    0;  Mismatches  129;  Indels   25;  Gaps    6;

Qy        911 TGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCATATCATTGTAA 970
              || ||||||  ||||| || || ||| || ||  ||||||||  ||    |      |||
```

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Db        120 TGATTATGGCAGTCTGGCTGGGAATGGTTCCATCAAGGCAAGGCTG---CAGGTCACTAA 176

Qy        971 CTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAATAATAATAAT 1030
              ||||||||||||||||  | | ||  || || | | || ||| |||| ||||||  |||
Db        177 CTAAAAAAGCTGACATCAAGCAAGGTATTTTATCCCCTGTCTGAAAAAAATAATGCTAAC 236

Qy       1031 GCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAA 1090
                 |           |||||    | ||||||| | | | |||| |||  |||| ||| |
Db        237 AGAA-----------AGAACATCCCATTTGCAACCAAGAACTAGCAGATTCTTTAAGGGA 285

Qy       1091 GAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAG 1150
              ||| |||||||  | ||| || || |     ||| ||| |||      |||||| |||||
Db        286 GAAATCAACAGCATATCTCCAACATTACCTGGAGTCAAACAA------GAAGTTTCCTAG 339

Qy       1151 ACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTG 1210
              ||||||   ||| || ||||| |   | ||  |||  |||  |   |||||||||||
Db        340 ACCAGAAACCATGAGCATCATCT---CCTTGGCTAATATATACATCAGTGGAGAAGGACA 396

Qy       1211 CAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCC-TTTTCTGGTT 1269
              || |||||||||||   | ||||||| ||  |||  ||| || |   || |||| || ||
Db        397 CA-CAGGCTCAAAGAGCTGAGTCATTACACCCAGATAACCAACTCCCCCTTTTTTTGATT 455

Qy       1270 TCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAG 1329
               | ||||||||| ||||| || |||||||  |||||| |||| |  ||||| | ||||||
Db        456 CCATGTTCACCAAGGAACTTTGTGATTATGATTAATCTTTCTCTACTGAATTTCCTAGAG 515

Qy       1330 AGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTGTTCTGGTTC 1389
               | |||||||||||  || | |  |||   || ||||||||||||||| |||||| ||||
Db        516 GGCTGCTGACCAACCAACATGTCATTCTACTTATGAATTAATAAACTGATGTTCTAGTTC 575


RESULT 11
CF106639
LOCUS       CF106639                 374 bp    mRNA    linear   EST 22-JUL-2003
DEFINITION  ZP0904D3 Pig liver cDNA Sus scrofa cDNA clone 04D3 similar to
            Coagulation Factor IX (F9), mRNA sequence.
ACCESSION   CF106639
VERSION     CF106639.1  GI:33145706
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Ernst,C.W., Raney,N.E., Martinez,M.M., Hargrave,K.M., Hill,G.M. and
            Link,J.B.
  TITLE     Identification of differentially expressed genes in pig liver
            tissue
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ernst CW
            Animal Science Molecular Genetics Lab
            Michigan State University
            B220 Anthony Hall, East Lansing, MI 48824, USA
            Tel: 517 432 1941
            Fax: 517 353 1699
            Email: ernstc@msu.edu
            PCR PRimers
            FORWARD: ACAATTTCACACAGGAGCTAGCAGAC
            BACKWARD: ACGACTCACTATAGGGCTTTTTTTTTTTTAC
            Insert Length: 374   Std Error: 0.00
            Seq primer: M13F
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..374
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="04D3"
                     /clone_lib="Pig liver cDNA"
ORIGIN

  Query Match             8.8%;  Score 149.6;  DB 6;  Length 374;
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  Best Local Similarity   75.8%;  Pred. No. 8.9e-22;
  Matches  226;  Conservative    0;  Mismatches   64;  Indels    8;  Gaps    3;

Qy          486 CATCAAAAACACTACTCCTTTTCCTCTACCC-TATTCCTCAATCTTTTACCTTTTCCAAA 544
                ||||| |||| || |  ||||  |  ||||| |  ||||  ||||  || |||| ||||
Db           20 CATCATAAACGCTGCATCTTTCTCGGTACCCTTGGTCCTGCATCTGCTATCTTTCCCAAC 79

Qy          545 TCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTCCATG 604
                ||| || |||||| |||||||||||||||||  ||||||| || || ||| || | | |
Db           80 TCCTAACCCCCAAGTCAGTTTTTCTCTTTCTCTCTCCCTCCCTGCCCTTTTCCTTTCCTA 139

Qy          605 GTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATACATG 664
                | | ||||||||| || |||||||||||| ||||| |||| ||||||||| | || ||
Db          140 GGCATTAAAGGAGGGAAGGGGAGCATCATACTGTTTTACTGCTGTACACAATGATGCAAA 199

Qy          665 TCTATCAAACCCAGACTTGCTTCCATAGTG----GAGACTTGCTTTTCAGAACATAGGGA 720
                 ||||||||||||| ||||||| ||   ||      |||||||| |||| | || |||||
Db          200 CCTATCAAACCCAGTCTTGCTTTCAATTTGTTCTTGGACTTGCTGTTCATAGCACAGGGA 259

Qy          721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATT 778
                ||||||||||||||||||    |||| ||||||||| || |  |||||| |  |||||
Db          260 TGAAGTAAGGTGCCTGAA---CTTGGAGGAAAAGTTCCTCTTGGAGAGTCACATTATT 314

RESULT 12
BX926315
LOCUS       BX926315                 688 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX926315 Sus Scrofa library (scan) Sus scrofa cDNA clone
            scan0021d.c.01 5prim, mRNA sequence.
ACCESSION   BX926315
VERSION     BX926315.1  GI:41143163
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0021  row: c  column: 1.
FEATURES             Location/Qualifiers
     source          1..688
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scan0021d.c.01"
                     /tissue_type="mixed"
                     /dev_stage="from embryos to adults"
                     /clone_lib="Sus Scrofa library (scan)"
                     /note="tissues: adipose tissue, brain, kidney, liver,
                     muscle, ovary, testis,  heart, hypothalamus, pancreas,
                     skin, spleen, thymus, placenta, pituitary  gland, seminal
                     vesicle, small intestine, uterus, adrenals, bulbo  uretral
                     gland, cerebral trunk, epididymis, female gonad,
                     gall-bladder,  hippocampus, large intestine, male gonad,
                     melanocytes, stomach, udder"
ORIGIN

  Query Match             8.8%;  Score 149.6;  DB 5;  Length 688;
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  Best Local Similarity   75.8%;  Pred. No. 9.1e-22;
  Matches  226;  Conservative    0;  Mismatches   64;  Indels    8;  Gaps    3;

Qy          486 CATCAAAAACACTACTCCTTTTCCTCTACCC-TATTCCTCAATCTTTTACCTTTTCCAAA 544
                ||||| |||| || |  ||||  |  ||||| |  ||||  ||||  || |||||||||
Db           21 CATCAGAAACGCTGCATCTTTCTCGGTACCCTTGGTCCTGCATCTGCTATCTTTTCCAAC 80

Qy          545 TCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTCCATG 604
                ||| || |||||| |||||||||||||||||  ||||||| || || ||| || | | |
Db           81 TCCTAACCCCCAAGTCAGTTTTTCTCTTTCTCTCTCCCTCCCTGCCCTTTTCCTTTCCTA 140

Qy          605 GTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATACATG 664
                | | ||||||||| || |||||||||||| ||||| |||| ||||||||| | || ||
Db          141 GGCATTAAAGGAGGGAAGGGGAGCATCATACTGTTTTACTGCTGTACACAATGATGCAAA 200

Qy          665 TCTATCAAACCCAGACTTGCTTCCATAGTG----GAGACTTGCTTTTCAGAACATAGGGA 720
                 ||||||||||||| ||||||| ||   ||      |||||||| |||| | ||  ||||
Db          201 CCTATCAAACCCAGTCTTGCTTTCAATTTGTTCTTGGACTTGCTGTTCATAGCACTGGGA 260

Qy          721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATT 778
                ||||||||||||||||||    |||| ||||||||| || |  |||||| |  |||||
Db          261 TGAAGTAAGGTGCCTGAA---CTTGGAGGAAAAGTTCCTCTTGGAGAGTCACATTATT 315

RESULT 13
BX925779
LOCUS       BX925779                 690 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX925779 Sus Scrofa library (scan) Sus scrofa cDNA clone
            scan0021d.o.01 5prim, mRNA sequence.
ACCESSION   BX925779
VERSION     BX925779.1  GI:41142627
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0021  row: o  column: 1.
FEATURES             Location/Qualifiers
     source          1..690
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scan0021d.o.01"
                     /tissue_type="mixed"
                     /dev_stage="from embryos to adults"
                     /clone_lib="Sus Scrofa library (scan)"
                     /note="tissues: adipose tissue, brain, kidney, liver,
                     muscle, ovary, testis,  heart, hypothalamus, pancreas,
                     skin, spleen, thymus, placenta, pituitary  gland, seminal
                     vesicle, small intestine, uterus, adrenals, bulbo  uretral
                     gland, cerebral trunk, epididymis, female gonad,
                     gall-bladder,  hippocampus, large intestine, male gonad,
                     melanocytes, stomach, udder"
ORIGIN

  Query Match             8.8%;  Score 149.6;  DB 5;  Length 690;
```

```
  Best Local Similarity   75.8%;  Pred. No. 9.1e-22;
  Matches  226;  Conservative    0;  Mismatches   64;  Indels    8;  Gaps    3;

Qy          486 CATCAAAAACACTACTCCTTTTCCTCTACCC-TATTCCTCAATCTTTTACCTTTTCCAAA 544
                ||||| |||| || |  ||||  |  ||||| |  ||||  ||||  || |||||||||
Db           21 CATCAGAAACGCTGCATCTTTCTCGGTACCCTTGGTCCTGCATCTGCTATCTTTTCCAAC 80

Qy          545 TCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTCCATG 604
                ||| || |||||| |||||||||||||||||  ||||||| || || ||| || | | |
Db           81 TCCTAACCCCCAAGTCAGTTTTTCTCTTTCTCTCTCCCTCCCTGCCCTTTTCCTTTCCTA 140

Qy          605 GTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATACATG 664
                | | ||||||||| || |||||||||||| ||||| |||| ||||||||| | || ||
Db          141 GGCATTAAAGGAGGGAAGGGGAGCATCATACTGTTTTACTGCTGTACACAATGATGCAAA 200

Qy          665 TCTATCAAACCCAGACTTGCTTCCATAGTG----GAGACTTGCTTTTCAGAACATAGGGA 720
                 ||||||||||||| ||||||| ||   ||      |||||||| |||| | ||  ||||
Db          201 CCTATCAAACCCAGTCTTGCTTTCAATTTGTTCTTGGACTTGCTGTTCATAGCACTGGGA 260

Qy          721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATT 778
                ||||||||||||||||||    |||| ||||||||| || |  |||||| |  |||||
Db          261 TGAAGTAAGGTGCCTGAA---CTTGGAGGAAAAGTTCCTCTTGGAGAGTCACATTATT 315


RESULT 14
CO775581
LOCUS       CO775581                 257 bp    mRNA    linear   EST 04-AUG-2004
DEFINITION  ILLUMIGEN_MCQ_52905 Katze_MFLV Macaca fascicularis cDNA clone
            IBIUW:29284 5' similar to Bases 5 to 157 highly similar to human F9
            (Hs.1330), mRNA sequence.
ACCESSION   CO775581
VERSION     CO775581.1  GI:50976844
KEYWORDS    EST.
SOURCE      Macaca fascicularis (crab-eating macaque)
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 257)
  AUTHORS   Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
            Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
            Iadonato,S.P.
  TITLE     Analysis of the Macaca mulatta transcriptome and the sequence
            divergence between Macaca and human
  JOURNAL   Genome Biol. 6 (7), R60 (2005)
   PUBMED   15998449
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.29. 411 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 257   Std Error: 0.00
            Plate: CL000540  row: A  column: 03
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..257
                     /organism="Macaca fascicularis"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9541"
                     /clone="IBIUW:29284"
                     /dev_stage="adult"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MFLV"
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                     /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN

  Query Match              8.6%;  Score 147;  DB 7;  Length 257;
  Best Local Similarity   93.9%;  Pred. No. 3.3e-21;
  Matches  153;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          617 GAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATACATGTCTATCAAACCC 676
                | ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db            3 GGGATGGGGAGCATCATTCTGTTATACTTCTGTACGCAGTTATACATGTCTATCAAACCC 62

Qy          677 AGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGATGAAGTAAGGTGCCTG 736
                |||||||||| |||||||||||||||||||||||||||||||||||||| || |||||||
Db           63 AGACTTGCTTTCATAGTGGAGACTTGCTTTTCAGAACATAGGGATGAAGCAACGTGCCTG 122

Qy          737 AAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTT 779
                |||| ||||||||||||||||||||||||||||||   ||| |
Db          123 AAAATTTTGGGGGAAAAGTTTCTTTCAGAGAGTTATTATATAT 165


RESULT 15
CO701325/c
LOCUS       CO701325                 400 bp    mRNA    linear   EST 26-JUL-2004
DEFINITION  DG32-1f6 DG32-liver Canis familiaris cDNA 3', mRNA sequence.
ACCESSION   CO701325
VERSION     CO701325.1  GI:50649993
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
            Henrich,J. and Loebbert,R.
  TITLE     Dog arrayTAG cDNA clone collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas Schlueter
            LION bioscience AG
            Waldhoferstrasse 98, D-69123 Heidelberg, Germany
            Tel: +49 6221 4038 150
            Fax: +49 6221 4038 290
            Email: Thomas.Schlueter@lionbioscience.com.
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         1281 ATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACC 1340
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Db          268 AACCTCTGCATGTACTTTAGTGTGTTAGGCTGGCTCCCTTTATGAATTAATAAACTGTTG 209
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                          GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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      Pred. No. is the number of results predicted by chance to have a
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                                ALIGNMENTS


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; Sequence 4, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 38059
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-328-925-4

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; Sequence 16994, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16994
;   LENGTH: 36755
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16994

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Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db       34144 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 34203

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34204 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 34263

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34264 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 34323

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34324 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 34383

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34384 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 34443

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34444 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 34503

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34504 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 34563

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34564 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 34623

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34624 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 34683

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34684 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 34743

Qy        1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34744 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 34803

Qy        1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       34804 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCCGCCAAGCTGCTGCCTTCTCC 34863

Qy        1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34864 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 34923

Qy        1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34924 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 34983

Qy        1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34984 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 35043

Qy        1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
               |||||||||||||||||||||  ||
Db       35044 GAGGTTAGGAGTTTCAGGCCAGCCT 35068


RESULT 3
US-09-053-871A-22
; Sequence 22, Application US/09053871A
; Patent No. 6315995
; GENERAL INFORMATION:
;  APPLICANT:  Pinsky, David J.
;  APPLICANT:  Stern, David
;  APPLICANT:  Rose, Eric
;  APPLICANT:  Solomon, Robert A.
;  APPLICANT:  Schmidt, Ann Marie
;  TITLE OF INVENTION:  METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
;  TITLE OF INVENTION:  STROKE OUTCOME
;  FILE REFERENCE:  51917-B
;  CURRENT APPLICATION NUMBER: US/09/053,871A
;  CURRENT FILING DATE:  1998-04-01
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2775
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-053-871A-22

  Query Match             81.5%;  Score 1391;  DB 3;  Length 2775;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1565 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1624

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1625 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1684

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1865 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1924

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1925 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1984

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1985 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2225 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2284

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2285 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2344

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2404

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2405 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2464

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2524

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2525 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2584

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2585 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2704

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2705 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2764

Qy        1381 TTCTGGTTCAT 1391
               |||||||||||
Db        2765 TTCTGGTTCAT 2775


RESULT 4
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US-10-133-907-2
; Sequence 2, Application US/10133907
; Patent No. 6677369
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth  R
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VI
;  TITLE OF INVENTION:  with vesicle vector
;  FILE REFERENCE: 6627-PA1170
;  CURRENT APPLICATION NUMBER: US/10/133,907
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: 60/286,314
;  PRIOR FILING DATE: 2001-04-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-133-907-2

  Query Match             81.5%;  Score 1391;  DB 3;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133
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Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Db        2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy        1381 TTCTGGTTCAT 1391
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Db        2794 TTCTGGTTCAT 2804
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RESULT 5
US-09-949-016-5252
; Sequence 5252, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5252
;   LENGTH: 2833
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5252
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  Query Match             81.4%;  Score 1389.4;  DB 3;  Length 2833;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1390;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1443 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1502

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1503 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1562

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1563 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1622

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1623 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1682

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1683 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1742

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1743 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1802

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1803 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1862

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1863 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1922

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1923 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1982

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1983 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2042

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2043 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2102

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        2103 CATGTCTATCAAACCCAGACTTGCTTCCGTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2162

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2163 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2222

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2223 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2282

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2283 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2342

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2343 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2402

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2403 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2462
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Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2463 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2522

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2523 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2582

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2583 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2642

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2643 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2702

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2703 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2762

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2763 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2822

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2823 TTCTGGTTCAT 2833


RESULT 6
US-09-118-748-1
; Sequence 1, Application US/09118748A
; Patent No. 6531298
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Darrel W.
;  APPLICANT: Chang, JinLi
;  TITLE OF INVENTION: Factor Ix Antihemophilic Factor with Increased Clotting
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 5470-183
;  CURRENT APPLICATION NUMBER: US/09/118,748A
;  CURRENT FILING DATE: 1998-07-17
;  EARLIER APPLICATION NUMBER: 60/053,571
;  EARLIER FILING DATE: 1997-07-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2792
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  sequence of
;   OTHER INFORMATION: human factor IX-R338A
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1400)
US-09-118-748-1

  Query Match             81.3%;  Score 1387.8;  DB 3;  Length 2792;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1389;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1461

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1521

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1581
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Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1641

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1701

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1761

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 TCTTCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1821

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1881

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1882 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1941

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2001

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2002 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2061

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2062 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2121

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2122 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2181

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2182 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2241

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2242 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2301

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2302 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2361

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2362 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2421

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2422 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2481

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       2482 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAACAGTGTTCAGAGCCAAGCAAGAAGTTGA 2541

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2542 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2601

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2602 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2661

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2662 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2721

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2722 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2781

Qy        1381 TTCTGGTTCAT 1391
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Db        2782 TTCTGGTTCAT 2792


RESULT 7
US-08-742-877-1
; Sequence 1, Application US/08742877
; Patent No. 6046380
;  GENERAL INFORMATION:
;    APPLICANT:  CLARK, Anthony J.
;    TITLE OF INVENTION:  DNA SEQUENCES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/742,877
;      FILING DATE:  01-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9408717.8
;      FILING DATE:  03-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLESHNER, RAZ E.
;      REGISTRATION NUMBER:  34,331
;      REFERENCE/DOCKET NUMBER:  0623.0470001/REF
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mRNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  30..1412
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  30..167
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  168..1412
US-08-742-877-1

  Query Match             81.2%;  Score 1385.8;  DB 3;  Length 2802;
  Best Local Similarity   68.2%;  Pred. No. 0;
  Matches  947;  Conservative  440;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||:||||||:||:::|||||||::||::||::||||::|||||::|||||||||:|:|||
Db        1414 AAUGAAAGAUGGAUUUCCAAGGUUAAUUCAUUGGAAUUGAAAAUUAACAGGGCCUCUCAC 1473

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               :|||:||:|||:::||||:|::::|::||||:::|||:|:|:|||::|:|:||:||::||:
Db        1474 UAACUAAUCACUUUCCCAUCUUUUGUUAGAUUUGAAUAUAUACAUUCUAUGAUCAUUGCU 1533

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ::::|:|:::|||||||||||:::||:|::::|||:|||||||::||::||||||:||||
Db        1534 UUUUCUCUUUACAGGGGAGAAUUUCAUAUUUUACCUGAGCAAAUUGAUUAGAAAAUGGAA 1593

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||:|||||||:|:||:|:|::||||||::||||:||:::|:|||||||||||||::||
Db        1594 CCACUAGAGGAAUAUAAUGUGUUAGGAAAUUACAGUCAUUUCUAAGGGCCCAGCCCUUGA 1653

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               |||||::|:||||::|||::|:||||:|:|:|||:||||:||:|:||::|:||||:|:||
Db        1654 CAAAAUUGUGAAGUUAAAUUCUCCACUCUGUCCAUCAGAUACUAUGGUUCUCCACUAUGG 1713

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||:|||:|||:|||::::|||:||::|||||||::|||:|::|||||:|::|:::||:
Db        1714 CAACUAACUCACUCAAUUUUCCCUCCUUAGCAGCAUUCCAUCUUCCCGAUCUUCUUUGCU 1773

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               :|:|||||||||||||:|||:|:::|::||::|:|:|:|||||:||||||:|:::||:|:||
Db        1774 UCUCCAACCAAAACAUCAAUGUUUAUUAGUUCUGUAUACAGUACAGGAUCUUUGGUCUAC 1833

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               :|:|:|||||||||||:|||||||:||:||||||||||||||||||:|||:|||||||:|
Db        1834 UCUAUCACAAGGCCAGUACCACACUCAUGAAGAAAGAACACAGGAGUAGCUGAGAGGCUA 1893

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||:||:|||||||||:||:||::::||:|:||||:|::||:|||:|::::|||::::|
Db        1894 AAACUCAUCAAAAACACUACUCCUUUUCCUCUACCCUAUUCCUCAAUCUUUUACCUUUUC 1953

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||:|||||:|||||||:|||:::::|:|:::|::||:|||:|:|:|||::::||||:|
Db        1954 CAAAUCCCAAUCCCCAAAUCAGUUUUUCUCUUUCUUACUCCCUCUCUCCCUUUUACCCUC 2013

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||:||:||::||||||||||:||||||||:||::|:|::|:||::|:|:||||||::|:|
Db        2014 CAUGGUCGUUAAAGGAGAGAUGGGGAGCAUCAUUCUGUUAUACUUCUGUACACAGUUAUA 2073

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||:|:|:|:|||||||||||::||::|||:||:|| |||::||::::|||||||:|||||
Db        2074 CAUGUCUAUCAAACCCAGACUUGCUUCCAUAGUGGGGACUUGCUUUUCAGAACAUAGGGA 2133

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               :||||:||||:|||:||||||:::||||||||||:::|:::|||||||::|||::|::::
Db        2134 UGAAGUAAGGUGCCUGAAAAGUUUGGGGGAAAAGUUUCUUUCAGAGAGUUAAGUUAUUUU 2193

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               |:|:|:|:||:|:|:|:|:||||:|:|:||:|:||||:|:|||:|:|:||:|:|:|:|:|
Db        2194 AUAUAUAUAAUAUAUAUAUAAAAUAUAUAAUAUACAAUAUAAAUAUAUAGUGUGUGUGUG 2253

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               :|:|||:|:|:|:|||||||||||||:|||||||:|:||:||||||||:||||||::|:|
Db        2254 UAUGCGUGUGUGUAGACACACACGCAUACACACAUAUAAUGGAAGCAAUAAGCCAUUCUA 2313

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               |||||::|:|:||::|:|||||:|:|||:|||||:||::: ||||||||||||::||||:
Db        2314 AGAGCUUGUAUGGUUAUGGAGGUCUGACUAGGCAUGAUUUGACGAAGGCAAGAUUGGCAU 2373

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               |:||::|:|||:||||||||:||||::||||||||||:|::|:||:|:::|:|||||:||
Db        2374 AUCAUUGUAACUAAAAAAGCUGACAUUGACCCAGACAUAUUGUACUCUUUCUAAAAAUAA 2433

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               :||:||:||:||:|||||||||||||||||||::||:::||||:|:|||||:||:|||||
Db        2434 UAAUAAUAAUGCUAACAGAAAGAAGAGAACCGUUCGUUUGCAAUCUACAGCUAGUAGAGA 2493

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               |:::|||||||||::||||||:|:|:|::||||||:|::|||||||||||||||||::||
Db        2494 CUUUGAGGAAGAAUUCAACAGUGUGUCUUCAGCAGUGUUCAGAGCCAAGCAAGAAGUUGA 2553

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||::|||:||||||||||||:|||:|:||:|:|:||:::|||:||||:||||||||||:|
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Db          2554 AGUUGCCUAGACCAGAGGACAUAAGUAUCAUGUCUCCUUUAACUAGCAUACCCCGAAGUG 2613

Qy          1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
                 ||||||||:|||||||||:||||||||:|||:||::||||:||||||||:|||::|:||:
Db          2614 GAGAAGGGUGCAGCAGGCUCAAAGGCAUAAGUCAUUCCAAUCAGCCAACUAAGUUGUCCU 2673

Qy          1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
                 :::|:||:::||:|::|||||:||||||::::||::|:||::||:||::|:|:|::|||:
Db          2674 UUUCUGGUUUCGUGUUCACCAUGGAACAUUUUGAUUAUAGUUAAUCCUUCUAUCUUGAAU 2733

Qy          1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
                 |::|:||||||::||:|||||||:||||:|:|:::|||:::|:|||::||:||||:||:|
Db          2734 CUUCUAGAGAGUUGCUGACCAACUGACGUAUGUUUCCCUUUGUGAAUUAAUAAACUGGUG 2793

Qy          1381 TTCTGGTTC 1389
                 ::|:||::|
Db          2794 UUCUGGUUC 2802
```

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RESULT 8
US-09-328-925-3
; Sequence 3, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-328-925-3

  Query Match             74.6%;  Score 1273;  DB 3;  Length 1273;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-308;
  Matches 1273;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy           111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy           171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy           231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy           291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy           351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy           411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy           471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy           531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy           591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy           651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy           711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy           771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy           831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy           891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy           951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy          1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy          1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy          1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy          1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy          1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy          1311 TATCTTGAATCTT 1323
                 |||||||||||||
Db          1261 TATCTTGAATCTT 1273
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RESULT 9
US-09-328-925-83
; Sequence 83, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 83
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-83

  Query Match             74.5%;  Score 1272;  DB 3;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-308;
  Matches 1272;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATG 60

Qy        112 ATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAG 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAG 120

Qy        172 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCC 180

Qy        232 AGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCT 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCT 240

Qy        292 CCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATC 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATC 300

Qy        352 TTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 360

Qy        412 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCT 420

Qy        472 GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT 480

Qy        532 TACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCT 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCT 540

Qy        592 TTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTAC 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTAC 600

Qy        652 ACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGA 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGA 660

Qy        712 ACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTA 720

Qy        772 AGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGT 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGT 780

Qy        832 GTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAA 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAA 840

Qy        892 GCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAA 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAA 900

Qy        952 GATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTC 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTC 960

Qy       1012 TAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGC 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGC 1020

Qy       1072 TAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCA 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCA 1080

Qy       1132 AGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAC 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAC 1140

Qy       1192 CCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTA 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTA 1200

Qy       1252 AGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCT 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCT 1260

Qy       1312 ATCTTGAATCTT 1323
              ||||||||||||
Db       1261 ATCTTGAATCTT 1272


RESULT 10
US-09-328-925-76
; Sequence 76, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-76

  Query Match             74.5%;  Score 1271.4;  DB 3;  Length 1273;
  Best Local Similarity   99.9%;  Pred. No. 4.1e-308;
  Matches 1272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTGACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300
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Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273

RESULT 11
US-09-328-925-77
; Sequence 77, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-77

  Query Match             74.5%;  Score 1271.4;  DB 3;  Length 1273;
  Best Local Similarity   99.9%;  Pred. No. 4.1e-308;
  Matches 1272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAAATTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy         831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy         891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy         951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy        1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy        1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy        1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy        1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy        1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy        1311 TATCTTGAATCTT 1323
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Db        1261 TATCTTGAATCTT 1273


RESULT 12
US-09-328-925-78
; Sequence 78, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-78

  Query Match             74.4%;  Score 1269.8;  DB 3;  Length 1273;
  Best Local Similarity   99.8%;  Pred. No. 1e-307;
  Matches 1271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy         111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy         171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy         231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy         291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy         351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy         411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy         471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy         531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy         591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
               |||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||
Db         541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGACGATCATTCTGTTATACTTCTGTA 600

Qy         651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy         711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy         771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy         831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy         891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy         951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy        1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy        1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy        1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy        1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy        1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273

RESULT 13
US-09-328-925-79
; Sequence 79, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-79

  Query Match             74.2%;  Score 1266.6;  DB 3;  Length 1273;
  Best Local Similarity   99.7%;  Pred. No. 6.5e-307;
  Matches 1269;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATGTACTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273

RESULT 14
US-09-328-925-82
; Sequence 82, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-82

  Query Match             73.9%;  Score 1261;  DB 3;  Length 1272;
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  Best Local Similarity   99.9%;  Pred. No. 1.6e-305;
  Matches 1272;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy         111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy         171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy         231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy         291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy         351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy         411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy         471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
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Qy         531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
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Db         481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy         591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy         651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy         711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
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Db         661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy         771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
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Db         721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy         831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
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Qy         891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy         951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
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Db        1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy        1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
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Db        1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy        1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
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Qy        1311 TATCTTGAATCTT 1323
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RESULT 15
US-09-328-925-80
; Sequence 80, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT: Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION: Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/09/328,925
;  CURRENT FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-328-925-80

  Query Match             73.9%;  Score 1261;  DB 3;  Length 1275;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-305;
  Matches 1273;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Search completed: April 18, 2006, 12:30:29
Job time : 365.148 secs
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            Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:46:08 ; Search time 1699.66 Seconds
                                           (without alignments)
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Title:          US-09-884-901A-7
Perfect score:  1707
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:      19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result              Query
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    2    1701.8      99.7  38059  3  US-09-880-107-2125          Sequence 2125, Ap
    3      1687      98.8  44752  8  US-10-741-600-17553         Sequence 17553, A
    4      1391      81.5   1400  9  US-10-956-157-5592          Sequence 5592, Ap
    5      1391      81.5   1400 10   US-11-060-756-1937          Sequence 1937, Ap
    6      1391      81.5   1400 10   US-11-060-756-6209          Sequence 6209, Ap
    7      1391      81.5   2804  5  US-10-132-829-2             Sequence 2, Appli
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    9      1391      81.5   2804  9  US-10-956-157-357           Sequence 357, App
   10      1391      81.5   2804  9  US-10-804-763-40            Sequence 40, Appl
   11    1387.8      81.3   2792  3  US-09-118-748-1             Sequence 1, Appli
   12      1377      80.7   2773  6  US-10-349-858-16            Sequence 16, Appl
   13    1376.6      80.6   2728  8  US-10-741-600-3             Sequence 3, Appli
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   18       236      13.8   1438  7  US-10-038-854-5             Sequence 5, Appli
   19     229.8      13.5    581  4  US-09-925-065A-808251       Sequence 808251,
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   21     200.6      11.8    201  8  US-10-741-600-2210          Sequence 2210, Ap
   22     200.6      11.8    201  8  US-10-741-600-2492          Sequence 2492, Ap
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   30      94.2       5.5    370  3  US-09-960-352-11540         Sequence 11540, A
   31        89       5.2    201  8  US-10-741-600-1867          Sequence 1867, Ap
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   34        89       5.2    201  8  US-10-741-600-2717          Sequence 2717, Ap
   35        89       5.2    201  8  US-10-741-600-18262         Sequence 18262, A
c  36      86.4       5.1    555  4  US-09-925-065A-308075       Sequence 308075,
   37      86.4       5.1   1758  4  US-09-925-065A-58792        Sequence 58792, A
c  38        86       5.0    528  4  US-09-925-065A-100582       Sequence 100582,
   39      85.4       5.0    473  3  US-09-814-353-18136         Sequence 18136, A
   40        85       5.0    201  8  US-10-741-600-1847          Sequence 1847, Ap
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   42        85       5.0    201  8  US-10-741-600-2411          Sequence 2411, Ap
   43        85       5.0    201  8  US-10-741-600-2697          Sequence 2697, Ap
   44        85       5.0    201  8  US-10-741-600-18236         Sequence 18236, A
c  45        84       4.9   2502  7  US-10-676-248B-37           Sequence 37, Appl

                               ALIGNMENTS


RESULT 1
US-09-884-901-7
; Sequence 7, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
;  APPLICANT: Miao, Carol
;  APPLICANT:  Kay, Mark
;  TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
;  FILE REFERENCE: UOFW-1-17396
;  CURRENT APPLICATION NUMBER: US/09/884,901
;  CURRENT FILING DATE:  2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/212,902
;  PRIOR FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 1707
;   TYPE: DNA
;   ORGANISM: HomoSapien
US-09-884-901-7

  Query Match             100.0%;  Score 1707;  DB 3;  Length 1707;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1707;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840

Qy          841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900

Qy          901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960

Qy          961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020

Qy         1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080

Qy         1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140

Qy         1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200

Qy         1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260

Qy         1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320

Qy         1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380

Qy         1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440

Qy         1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500

Qy         1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560

Qy         1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620

Qy         1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680

Qy         1681 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707
                |||||||||||||||||||||||||||
Db         1681 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707


RESULT 2
US-09-880-107-2125
; Sequence 2125, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2125
;   LENGTH: 38059
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 K02402
US-09-880-107-2125

  Query Match             99.7%;  Score 1701.8;  DB 3;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy            1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy           61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy          121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34453 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 34512

Qy          181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572

Qy          241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632
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Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34693 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 34752

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34753 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 34812

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34813 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 34872

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34873 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 34932

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34933 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 34992

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34993 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 35052

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35053 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 35112

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35113 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 35172

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35233 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 35292

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35293 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 35352

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35353 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35413 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 35472

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 35592

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 35652

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35653 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 35712

Qy       1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35713 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 35772

Qy       1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35773 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 35832

Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35833 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 35892

Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35953 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 36012

Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||  ||
Db      36013 GAGGTTAGGAGTTTCAGGCCAGCCT 36037


RESULT 3
US-10-741-600-17553
; Sequence 17553, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17553
;   LENGTH: 44752
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(44752)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-741-600-17553

  Query Match             98.8%;  Score 1687;  DB 8;  Length 44752;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1699;  Conservative    2;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37365 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 37424

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37425 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 37484

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37485 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 37544

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37545 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 37604

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37605 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 37664

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37665 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 37724

Qy           361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37725 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 37784

Qy           421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37785 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 37844

Qy           481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37845 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 37904

Qy           541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37905 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 37964

Qy           601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37965 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 38024

Qy           661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
                 ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db         38025 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 38084

Qy           721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38085 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 38144

Qy           781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
                 |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db         38145 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 38202

Qy           841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38203 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 38262

Qy           901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38263 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 38322

Qy           961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38323 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 38382

Qy          1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38383 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 38442

Qy          1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38443 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 38502

Qy          1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38503 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 38562

Qy          1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38563 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 38622

Qy          1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38623 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 38682

Qy          1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38683 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 38742

Qy          1381 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         38743 TTCTGGTTCATACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 38802

Qy          1441 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCTGCCTTCTCC 1500
                 |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         38803 TGATGATGCATGGGACTACTGACAAAATCACTCTGACCCYGCCAAGCTGCTGCCTTCTCC 38862

Qy          1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38863 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 38922

Qy          1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38923 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 38982

Qy          1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38983 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 39042

Qy          1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
                 |||||||||||||||||||||  ||
Db         39043 GAGGTTAGGAGTTTCAGGCCAGCCT 39067


RESULT 4
US-10-956-157-5592
; Sequence 5592, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5592
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-956-157-5592

  Query Match             81.5%;  Score 1391;  DB 9;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy             1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            10 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 69

Qy            61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            70 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 129

Qy           121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           130 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 189

Qy           181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           190 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 249

Qy           241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           250 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 309

Qy           301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           310 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 369

Qy           361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         370 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 429

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 489

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         490 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 549

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         550 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 609

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         610 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 669

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         670 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 729

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         730 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 789

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         790 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 849

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         850 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 909

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         910 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 969

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         970 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1029

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1030 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1089

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1090 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1149

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1150 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1209

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1210 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1269

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1270 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1329

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1330 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1389

Qy        1381 TTCTGGTTCAT 1391
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Db        1390 TTCTGGTTCAT 1400
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RESULT 5
US-11-060-756-1937

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; Sequence 1937, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1937
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-1937

  Query Match             81.5%;  Score 1391;  DB 10;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          10 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 69

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          70 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 129

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         130 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 189

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 249

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 309

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         310 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 369

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 429

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 489

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         490 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 549

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         550 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 609

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         610 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 669

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         670 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 729

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         730 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 789
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Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 849

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 909

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 969

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1029

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1089

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1149

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1209

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1269

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1329

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1389

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       1390 TTCTGGTTCAT 1400


RESULT 6
US-11-060-756-6209
; Sequence 6209, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6209
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-6209

  Query Match             81.5%;  Score 1391;  DB 10;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 69

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 129

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 189

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 249

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 309

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 369

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 429

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 489

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 549

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 609

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 669

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 729

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 789

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 849

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 909

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 969

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1029

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1089

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1149
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Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1150 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1209

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1210 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1269

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1270 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1329

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1330 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1389

Qy        1381 TTCTGGTTCAT 1391
               |||||||||||
Db        1390 TTCTGGTTCAT 1400


RESULT 7
US-10-132-829-2
; Sequence 2, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth  R
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
;  TITLE OF INVENTION:  with vesicle vector
;  FILE REFERENCE: 6627-PA1170
;  CURRENT APPLICATION NUMBER: US/10/132,829
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: 60/286,314
;  PRIOR FILING DATE: 2001-04-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-132-829-2

  Query Match             81.5%;  Score 1391;  DB 5;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy        1381 TTCTGGTTCAT 1391
               |||||||||||
Db        2794 TTCTGGTTCAT 2804


RESULT 8
US-10-133-907-2
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; Sequence 2, Application US/10133907
; Publication No. US20030195223A1
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth  R
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
;  TITLE OF INVENTION:  with vesicle vector
;  FILE REFERENCE: 6627-PA1170
;  CURRENT APPLICATION NUMBER: US/10/133,907
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: 60/286,314
;  PRIOR FILING DATE: 2001-04-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-133-907-2

  Query Match             81.5%;  Score 1391;  DB 6;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2794 TTCTGGTTCAT 2804


RESULT 9
US-10-956-157-357
; Sequence 357, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
;   LENGTH: 2804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-956-157-357

  Query Match             81.5%;  Score 1391;  DB 9;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy           61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy          121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy          181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy          241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy          301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773

Qy          361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy          421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy          481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy          541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy          601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy          661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy          721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy          781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy          841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy          901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy          961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy         1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy         1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy         1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy         1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy         1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy         1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy         1381 TTCTGGTTCAT 1391
                |||||||||||
Db         2794 TTCTGGTTCAT 2804


RESULT 10
US-10-804-763-40
; Sequence 40, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
;  APPLICANT: Qi, Yan
;  APPLICANT:  Zhang, Xianghua
;  APPLICANT:  Konigsberg, Paula
;  TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
;  FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
;  CURRENT APPLICATION NUMBER: US/10/804,763
;  CURRENT FILING DATE:  2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/456,378
;  PRIOR FILING DATE: 2003-03-19
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 2804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-804-763-40

  Query Match             81.5%;  Score 1391;  DB 9;  Length 2804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1414 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1473

Qy           61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1474 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1533

Qy          121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1534 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1593

Qy          181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1594 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653

Qy          241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1654 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1713

Qy          301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1714 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1773
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Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1833

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1953

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2013

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2133

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2193

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2253

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2313

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2373

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2433

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2493

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2553

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2613

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2673

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2733

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2793

Qy       1381 TTCTGGTTCAT 1391
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Db       2794 TTCTGGTTCAT 2804
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RESULT 11
US-09-118-748-1
; Sequence 1, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Darrel W.
;  APPLICANT: Chang, JinLi
;  TITLE OF INVENTION: Factor Ix Antihemophilic Factor with Increased Clotting
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 5470-183
;  CURRENT APPLICATION NUMBER: US/09/118,748A
;  CURRENT FILING DATE: 1998-07-17
;  EARLIER APPLICATION NUMBER: 60/053,571
;  EARLIER FILING DATE: 1997-07-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2792
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  sequence of
;   OTHER INFORMATION: human factor IX-R338A
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1400)
US-09-118-748-1

  Query Match             81.3%;  Score 1387.8;  DB 3;  Length 2792;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1389;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1461

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1521

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1581

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1641

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1701

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1761

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 TCTTCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1821

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1881

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db       1882 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1941

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2001

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db  2002 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2061

Qy   661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2062 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2121

Qy   721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2122 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2181

Qy   781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2182 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2241

Qy   841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2242 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2301

Qy   901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2302 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2361

Qy   961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2362 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2421

Qy  1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2422 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2481

Qy  1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  2482 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAACAGTGTTCAGAGCCAAGCAAGAAGTTGA 2541

Qy  1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2542 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2601

Qy  1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2602 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2661

Qy  1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2662 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2721

Qy  1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2722 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2781

Qy  1381 TTCTGGTTCAT 1391
         |||||||||||
Db  2782 TTCTGGTTCAT 2792


RESULT 12
US-10-349-858-16
; Sequence 16, Application US/10349858
; Publication No. US20030220247A1
; GENERAL INFORMATION:
;  APPLICANT: The Children's Hospital of Philadelphia
;  APPLICANT:  HIGH, KATHERINE A.
;  APPLICANT:  CAMIRE, RODNEY M.
;  APPLICANT:  LARSON, PETER J.
;  APPLICANT:  STAFFORD, DARREL W.
;  TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C
;  TITLE OF INVENTION:  FACTORS
;  FILE REFERENCE: 018743-0301425
;  CURRENT APPLICATION NUMBER: US/10/349,858
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 09/526,947
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/124,609
;  PRIOR FILING DATE: 1999-03-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 2773
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-349-858-16

  Query Match             80.7%;  Score 1377;  DB 6;  Length 2773;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1389;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy     1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444

Qy    61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504

Qy   121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1505 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1564

Qy   181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1565 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1624

Qy   241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1625 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1684

Qy   301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1685 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744

Qy   361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1745 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1804

Qy   421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1805 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864

Qy   481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1865 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1924

Qy   541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1925 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1984

Qy   601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1985 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044

Qy   661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104

Qy   721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2105 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2164

Qy   781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2165 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2224

Qy   841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2225 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2284
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Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2285 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2344

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        2345 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCT--AAATAA 2402

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2403 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2462

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2463 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2522

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2523 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2582

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2583 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2642

Qy        1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2643 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2702

Qy        1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2703 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2762

Qy        1381 TTCTGGTTCAT 1391
               |||||||||||
Db        2763 TTCTGGTTCAT 2773


RESULT 13
US-10-741-600-3
; Sequence 3, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 2728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2728)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-3

  Query Match             80.6%;  Score 1376.6;  DB 8;  Length 2728;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy           1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1340 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1399

Qy          61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1400 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1459
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Qy         121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1460 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1519

Qy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1520 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1579

Qy         241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1580 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1639

Qy         301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1640 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1699

Qy         361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1700 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1759

Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1760 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1819

Qy         481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1820 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1879

Qy         541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1880 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1939

Qy         601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1940 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 1999

Qy         661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
               ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        2000 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2059

Qy         721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2060 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2119

Qy         781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
               |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        2120 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2177

Qy         841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2178 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2237

Qy         901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2238 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2297

Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2298 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2357

Qy        1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2358 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2417

Qy        1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2418 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2477

Qy        1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2478 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2537

Qy        1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2538 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2597

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2598 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2657

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2658 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2717

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2718 TTCTGGTTCAT 2728


RESULT 14
US-10-741-600-1
; Sequence 1, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2771
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2771)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-1

  Query Match             80.6%;  Score 1376.6;  DB 8;  Length 2771;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1442

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1502

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1562

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1622

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1682

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1742

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1802

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1862

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1922

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1982

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2042

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2043 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2102

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2162

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2163 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2220

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2280

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2340

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2400

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 2460

Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 2520

Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 2580

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2640

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2700

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2760

Qy       1381 TTCTGGTTCAT 1391
              |||||||||||
Db       2761 TTCTGGTTCAT 2771


RESULT 15
US-10-741-600-2
; Sequence 2, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
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;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 2777
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2777)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-2

  Query Match             80.6%;  Score 1376.6;  DB 8;  Length 2777;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1388;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1448

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1508

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1509 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1568

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1628

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1629 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1688

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1689 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1748

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1749 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1808

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1868

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1869 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1928

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1929 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1988

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
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Db       1989 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2048

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       2049 CATGTCTATCAAACCCAGACTTGCTTCCRTAGTGGAGACTTGCTTTTCAGAACATAGGGA 2108

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2109 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2168

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
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Db       2169 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATA--GTGTGTGTG 2226

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       2287 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2346

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db       2347 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2406

Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Qy       1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGA 1140
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Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
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Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Db       2587 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2646

Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Db       2647 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2706

Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Db       2707 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2766

Qy       1381 TTCTGGTTCAT 1391
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Db       2767 TTCTGGTTCAT 2777

Search completed: April 18, 2006, 13:17:15
Job time : 1704.66 secs
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          April 18, 2006, 12:50:18 ; Search time 1048.42 Seconds
                                            (without alignments)
                                            6557.999 Million cell updates/sec

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Perfect score:   1707
Sequence:        1 aatgaaagatggatttccaa..........ggagtttcaggccaagctta 1707

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters:      18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_NA_New:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                    %
Result              Query
  No.     Score     Match Length DB   ID                       Description
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     1   1701.8    99.7  38059  11  US-11-129-861-4           Sequence 4, Appli
     2     1273    74.6   1273  11  US-11-129-861-3           Sequence 3, Appli
     3     1272    74.5   1272  11  US-11-129-861-83          Sequence 83, Appl
     4   1271.4    74.5   1273  11  US-11-129-861-76          Sequence 76, Appl
     5   1271.4    74.5   1273  11  US-11-129-861-77          Sequence 77, Appl
     6   1269.8    74.4   1273  11  US-11-129-861-78          Sequence 78, Appl
     7   1266.6    74.2   1273  11  US-11-129-861-79          Sequence 79, Appl
     8     1261    73.9   1272  11  US-11-129-861-82          Sequence 82, Appl
     9     1261    73.9   1275  11  US-11-129-861-80          Sequence 80, Appl
    10     1260    73.8   1276  11  US-11-129-861-81          Sequence 81, Appl
    11     1027    60.2   1400  14  US-11-128-061-3654        Sequence 3654, Ap
    12     1027    60.2   1400  14  US-11-128-049-3654        Sequence 3654, Ap
    13     1027    60.2   2458  14  US-11-128-061-12          Sequence 12, Appl
    14     1027    60.2   2458  14  US-11-128-049-12          Sequence 12, Appl
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    16       89     5.2    101  11  US-11-129-861-58          Sequence 58, Appl
c   17     86.4     5.1    548  10  US-10-301-480-383882      Sequence 383882,
c   18     86.4     5.1    548  10  US-10-301-480-997291      Sequence 997291,
c   19     86.4     5.1    555   6  US-09-925-065A-308075    Sequence 308075,
    20     86.4     5.1   1758   6  US-09-925-065A-58792     Sequence 58792, A
    21     86.4     5.1   1758   9  US-10-301-480-160030     Sequence 160030,
    22     86.4     5.1   1758  10  US-10-301-480-773439      Sequence 773439,
c   23       86     5.0    528   6  US-09-925-065A-100582    Sequence 100582,
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c   37       84     4.9   1047   9  US-10-301-480-38557      Sequence 38557, A
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c   41       84     4.9   1047  10  US-10-301-480-651965      Sequence 651965,
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    44     83.8     4.9    521  10  US-10-301-480-417357      Sequence 417357,
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                                  ALIGNMENTS


RESULT 1
US-11-129-861-4
; Sequence 4, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 38059
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-129-861-4

  Query Match             99.7%;  Score 1701.8;  DB 11;  Length 38059;
  Best Local Similarity   99.9%;  Pred. No. 3.3e-85;
  Matches 1703;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
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Db      34333 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 34392

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
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Db      34393 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 34452

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Db      34513 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 34572
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Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Db      34573 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Db      34633 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 34692

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
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Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
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Db      35173 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 35232

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Qy       1021 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080
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Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532

Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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Qy       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380
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Qy       1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560
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Qy       1561 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 1620
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Db      35893 AATATATTTTTGTCTTCGCATATAAGTATAAATAAACATATTTTTAAATTTCTTGGCTGG 35952

Qy       1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680
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Qy       1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705
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RESULT 2
US-11-129-861-3
; Sequence 3, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-129-861-3

  Query Match             74.6%;  Score 1273;  DB 11;  Length 1273;
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  Matches 1273;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
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Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

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Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
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Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
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Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273


RESULT 3
US-11-129-861-83
; Sequence 83, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-83

  Query Match             74.5%;  Score 1272;  DB 11;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-61;
  Matches 1272;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATG 60

Qy        112 ATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAG 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAG 120

Qy        172 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCC 180

Qy        232 AGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCT 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCT 240

Qy        292 CCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATC 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATC 300

Qy        352 TTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 360

Qy        412 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCT 420

Qy        472 GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT 480

Qy        532 TACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCT 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCT 540

Qy        592 TTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTAC 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTAC 600

Qy        652 ACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGA 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGA 660

Qy        712 ACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTA 720
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Qy        772 AGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGT 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGT 780

Qy        832 GTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAA 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAA 840

Qy        892 GCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAA 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAA 900

Qy        952 GATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTC 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTC 960

Qy       1012 TAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGC 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGC 1020

Qy       1072 TAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCA 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCA 1080

Qy       1132 AGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAC 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAC 1140

Qy       1192 CCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTA 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTA 1200

Qy       1252 AGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCT 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCT 1260

Qy       1312 ATCTTGAATCTT 1323
              ||||||||||||
Db       1261 ATCTTGAATCTT 1272


RESULT 4
US-11-129-861-76
; Sequence 76, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-76

  Query Match              74.5%;  Score 1271.4;  DB 11;  Length 1273;
  Best Local Similarity   99.9%;  Pred. No. 2.2e-61;
  Matches 1272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTGACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60
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Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140
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Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273


RESULT 5
US-11-129-861-77
; Sequence 77, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-77

  Query Match             74.5%;  Score 1271.4;  DB 11;  Length 1273;
  Best Local Similarity   99.9%;  Pred. No. 2.2e-61;
  Matches 1272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAAATTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273


RESULT 6
US-11-129-861-78
; Sequence 78, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 78
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-78

  Query Match              74.4%;  Score 1269.8;  DB 11;  Length 1273;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-61;
  Matches 1271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGACGATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273


RESULT 7
US-11-129-861-79
; Sequence 79, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-79

  Query Match              74.2%;  Score 1266.6;  DB 11;  Length 1273;
  Best Local Similarity   99.7%;  Pred. No. 4e-61;
  Matches 1269;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATGTACTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1260

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1261 TATCTTGAATCTT 1273

RESULT 8
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US-11-129-861-82
; Sequence 82, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-82

  Query Match             73.9%;  Score 1261;  DB 11;  Length 1272;
  Best Local Similarity   99.9%;  Pred. No. 8e-61;
  Matches 1272;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1201 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTT-ATCCTTC 1259

Qy       1311 TATCTTGAATCTT 1323
              |||||||||||||
Db       1260 TATCTTGAATCTT 1272


RESULT 9
US-11-129-861-80
; Sequence 80, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-80

  Query Match             73.9%;  Score 1261;  DB 11;  Length 1275;
  Best Local Similarity   99.8%;  Pred. No. 8e-61;
  Matches 1273;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGA- 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        350 -TCTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA 408
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA 360

Qy        409 TCTTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTA 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTA 420

Qy        469 GCTGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATC 480

Qy        529 TTTTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTC 540

Qy        589 CCTTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTG 600

Qy        649 TACACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTC 660

Qy        709 AGAACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGAACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAG 720

Qy        769 TTAAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATAT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTAAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATAT 780

Qy        829 AGTGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAA 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAA 840

Qy        889 TAAGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGG 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TAAGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGG 900

Qy        949 CAAGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCT 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCT 960

Qy       1009 TTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTAC 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTAC 1020

Qy       1069 AGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAA 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAA 1080

Qy       1129 GCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCA 1140
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Qy       1189 TACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAA 1248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAA 1200

Qy       1249 CTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCT 1260

Qy       1309 TCTATCTTGAATCTT 1323
              |||||||||||||||
Db       1261 TCTATCTTGAATCTT 1275


RESULT 10
US-11-129-861-81
; Sequence 81, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
;  APPLICANT: Kurachi, Kotoku
;  APPLICANT:  Kurachi, Sumiko
;  TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: UM-03603
;  CURRENT APPLICATION NUMBER: US/11/129,861
;  CURRENT FILING DATE:  2005-05-16
;  PRIOR APPLICATION NUMBER: US/09/328,925
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
;   LENGTH: 1276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-11-129-861-81

  Query Match             73.8%;  Score 1260;  DB 11;  Length 1276;
  Best Local Similarity   99.8%;  Pred. No. 9e-61;
  Matches 1273;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy         51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT 60

Qy        111 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120

Qy        171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180

Qy        231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 240

Qy        291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 300

Qy        351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy        411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420

Qy        471 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480

Qy        531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540

Qy        591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA 600

Qy        651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 660

Qy        711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720

Qy        771 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTTATTTTATATATATAATATATATATAAAATATATAATATACAATATAAATATATAG 780

Qy        831 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 840

Qy        891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900

Qy        951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

Qy       1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAG 1020

Qy       1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080

Qy       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1140

Qy       1191 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAA-- 1248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1200

Qy       1249 -CTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCC 1307
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCC 1260

Qy       1308 TTCTATCTTGAATCTT 1323
              ||||||||||||||||
Db       1261 TTCTATCTTGAATCTT 1276


RESULT 11
US-11-128-061-3654
; Sequence 3654, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
;  TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
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;  FILE REFERENCE: 01997.027701
;  CURRENT APPLICATION NUMBER: US/11/128,061
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ,ID NO 3654
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-128-061-3654

  Query Match             60.2%;  Score 1027;  DB 14;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-48;
  Matches 1027;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 480

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 540

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 600

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 660

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 720

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 780

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 840

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 900

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 960

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 1020

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 1080

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 1140

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 1200
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Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 1260

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 1320

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1380

Qy       1021 TAATAAT 1027
              |||||||
Db       1381 TAATAAT 1387


RESULT 12
US-11-128-049-3654
; Sequence 3654, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FO
;  TITLE OF INVENTION:  MAKING AND USING SAME
;  FILE REFERENCE: 01997.027700
;  CURRENT APPLICATION NUMBER: US/11/128,049
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3654
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-128-049-3654

  Query Match             60.2%;  Score 1027;  DB 14;  Length 1400;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-48;
  Matches 1027;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 480

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 540

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 600

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 660

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 720
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Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 780

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 840

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 900

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 960

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 1020

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       1021 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 1080

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       1081 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 1140

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 1200

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db       1201 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 1260

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       1261 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 1320

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1380

Qy       1021 TAATAAT 1027
              |||||||
Db       1381 TAATAAT 1387


RESULT 13
US-11-128-061-12
; Sequence 12, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
;  TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
;  FILE REFERENCE: 01997.027701
;  CURRENT APPLICATION NUMBER: US/11/128,061
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 2458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-128-061-12

  Query Match             60.2%;  Score 1027;  DB 14;  Length 2458;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-48;
  Matches 1027;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1478

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1538

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1598

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1658

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1718

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1778

Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1779 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1838

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1898

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1958

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2018

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2078

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
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Db       2079 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2138

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2198

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2258

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db       2259 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2318

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
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Db       2319 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2378

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
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Db       2379 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2438

Qy       1021 TAATAAT 1027
              |||||||
Db       2439 TAATAAT 2445


RESULT 14
US-11-128-049-12
; Sequence 12, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
;  TITLE OF INVENTION:  MAKING AND USING SAME
;  FILE REFERENCE: 01997.027700
;  CURRENT APPLICATION NUMBER: US/11/128,049
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 2458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-128-049-12

  Query Match             60.2%;  Score 1027;  DB 14;  Length 2458;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-48;
  Matches 1027;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1478

Qy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1538

Qy        121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1598

Qy        181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240
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Db       1599 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1658

Qy        241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300
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Db       1659 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1718

Qy        301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360
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Qy        361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420
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Db       1779 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 1838

Qy        421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1898

Qy        481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1958

Qy        541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2018

Qy        601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2078

Qy        661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2138

Qy        721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780
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Db       2139 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 2198

Qy        781 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 ATATATATAATATATATATAAAATATATAATATACAATATAAATATATAGTGTGTGTGTG 2258

Qy        841 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900
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Db       2259 TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 2318

Qy        901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 2378

Qy        961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 2438

Qy       1021 TAATAAT 1027
              |||||||
Db       2439 TAATAAT 2445


RESULT 15
US-09-925-065A-808251
; Sequence 808251, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 808251
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-808251

  Query Match             13.5%;  Score 229.8;  DB 6;  Length 581;
  Best Local Similarity   99.1%;  Pred. No. 2.8e-05;
  Matches  231;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       1473 CTGACCCTGCCAAGCTGCTGCCTTCTCCTGCCCCAACCTCACCCCCAGCCAGGCCTCACT 1532
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Db          1 CTGACCCTGCCAAGCTGCTGCCTTCTCCTGCCCCAACCTCACCCCCAGCCAGGCCTCACT 60

Qy       1533 CTTGCTAGTTCCTTTAGTTCTTTTAGTCAATATATTTTTGTCTTCGCATATAAGTATAAA 1592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTGCTAGTTCCTTTAGTTCTTTTAGTCAATATATTTTTGTCTTCGCATATAAGTATAAA 120

Qy       1593 TAAACATATTTTTAAATTTCTTGGCTGGGCCCAGTGGCTCACGCCTATAATCCCAGCACT 1652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAACATATTTTTAAATTTCTTGGCTGGGCCCAGTGGCTCACGCCTATAATCCCAGCACT 180

Qy       1653 TCTGGAGGCCAAGGTGGGCGGATCACCTGAGGTTAGGAGTTTCAGGCCAAGCT 1705
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        181 TCTGGAGGCCAAGGTGGGCGGATCACCTGAGGTTAGGAGTTTCAGGCCAGCCT 233

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Job time : 1049.42 secs
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                      GenCore version 5.1.7
          Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:06:40 ; Search time 844.062 Seconds
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Title:          US-09-884-901A-8
Perfect score:  154
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                Gapop 10.0 , Gapext 1.0

Searched:       5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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                2:  gb_in:*
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                10:  gb_sts:*
                11:  gb_sy:*
                12:  gb_un:*
                13:  gb_vi:*
                14:  gb_htg:*
                15:  gb_pl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                      %
Result              Query
  No.     Score     Match Length DB  ID                       Description
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     1      154     100.0    154  6  AX379349                 AX379349 Sequence
     2      154     100.0    328  6  AX379350                 AX379350 Sequence
     3      154     100.0    771  6  AX379345                 AX379345 Sequence
     4      154     100.0    774  8  HSU32510                 U32510 Human apoli
     5      154     100.0  41907  6  AX358722                 AX358722 Sequence
     6      154     100.0  41907  8  AF050154                 AF050154 Homo sapi
     7      154     100.0 107567  8  AC011481                 AC011481 Homo sapi
     8      142      92.2 208239 14   AC021988                 AC021988 Homo sapi
     9    141.2      91.7  39483 14   AC146473                 AC146473 Hylobates
    10    139.6      90.6 183798 14   AC145523                 AC145523 Papio ham
    11    136.4      88.6 231234 14   AC148222                 AC148222 Colobus g
    12    131.6      85.5   4097  8  HSU35114                 U35114 Human apoli
c   13    131.6      85.5  63931 14   AC120211                 AC120211 Pan trogl
c   14      130      84.4 183798 14   AC145523                 AC145523 Papio ham
    15    114.4      74.3 185724 14   AC146285                 AC146285 Callicebu
    16    112.8      73.2 191327 14   AC151887                 AC151887 Saimiri b
    17    111.4      72.3 186842 14   AC146283                 AC146283 Callithri
    18    111.2      72.2 193027 14   AC146520                 AC146520 Aotus nan
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c   19    104.2      67.7 183536 14   AC135911                 AC135911 Lemur cat
    20       82      53.2     90  6  AR595858                 AR595858 Sequence
    21       82      53.2     90  6  AR595862                 AR595862 Sequence
c   22       78      50.6     82  6  AR595864                 AR595864 Sequence
c   23       77      50.0     82  6  AR595860                 AR595860 Sequence
c   24     76.4      49.6 221553  9  AC149282                 AC149282 Mus muscu
c   25     76.4      49.6 228698 14   AC127479                 AC127479 Mus muscu
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c   27       74      48.1     78  6  AR595861                 AR595861 Sequence
c   28       74      48.1     78  6  AR595865                 AR595865 Sequence
    29     73.2      47.5 263682 14   AC120709                 AC120709 Rattus no
    30       70      45.5     70  6  AR595863                 AR595863 Sequence
    31       69      44.8     70  6  AR595859                 AR595859 Sequence
c   32     37.4      24.3 210122 14   AC108618                 AC108618 Rattus no
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c   34     37.4      24.3 306529 14   AC109083                 AC109083 Rattus no
    35     35.2      22.9 214674 14   AC164341                 AC164341 Bos tauru
c   36       35      22.7 135384  4  AC152565                 AC152565 Ornithorh
    37       35      22.7 204375 14   AC117045                 AC117045 Rattus no
c   38       35      22.7 225735 14   AC106386                 AC106386 Rattus no
    39     34.8      22.6 139711 14   AC153093                 AC153093 Ornithorh
    40     34.8      22.6 158972 14   AC160538                 AC160538 Mus muscu
c   41     34.8      22.6 184010  9  AC113976                 AC113976 Mus muscu
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    43     34.8      22.6 230167 14   AC097156                 AC097156 Rattus no
    44     34.4      22.3 222164  9  AC109153                 AC109153 Mus muscu
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                                   ALIGNMENTS

RESULT 1
AX379349
LOCUS       AX379349                 154 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 8 from Patent WO0198482.
ACCESSION   AX379349
VERSION     AX379349.1  GI:19575189
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Miao,C.H. and Kay,M.A.
  TITLE     Liver-specific gene expression cassettes, and methods of use
  JOURNAL   Patent: WO 0198482-A 8 27-DEC-2001;
            The Board of Trustees of The Leland Stanford Junior University (US)
            ; The University of Washington (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Db          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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RESULT 2
AX379350
LOCUS       AX379350                 328 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 9 from Patent WO0198482.
ACCESSION   AX379350
VERSION     AX379350.1  GI:19575190
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Miao,C.H. and Kay,M.A.
  TITLE     Liver-specific gene expression cassettes, and methods of use
  JOURNAL   Patent: WO 0198482-A 9 27-DEC-2001;
            The Board of Trustees of The Leland Stanford Junior University (US)
            ; The University of Washington (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.5e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db        138 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 197

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db        198 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 231


RESULT 3
AX379345
LOCUS       AX379345                 771 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 4 from Patent WO0198482.
ACCESSION   AX379345
VERSION     AX379345.1  GI:19575185
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Miao,C.H. and Kay,M.A.
  TITLE     Liver-specific gene expression cassettes, and methods of use
  JOURNAL   Patent: WO 0198482-A 4 27-DEC-2001;
            The Board of Trustees of The Leland Stanford Junior University (US)
            ; The University of Washington (US)
FEATURES             Location/Qualifiers
     source          1..771
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 154;  DB 6;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Db         78 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 137

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db        138 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 197

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        198 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 231


RESULT 4
HSU32510
LOCUS       HSU32510                 774 bp    DNA     linear   PRI 31-JAN-1996
DEFINITION  Human apolipoprotein E/C-I gene locus, hepatic control region
            HCR-1.
ACCESSION   U32510
VERSION     U32510.1  GI:975886
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   Dang,Q., Walker,D., Taylor,S., Allan,C., Chin,P., Fan,J. and
            Taylor,J.
  TITLE     Structure of the hepatic control region of the human apolipoprotein
            E/C-I gene locus
  JOURNAL   J. Biol. Chem. 270 (38), 22577-22585 (1995)
   PUBMED   7673250
REFERENCE   2  (bases 1 to 774)
  AUTHORS   Dang,Q., Walker,D., Taylor,S., Allan,C., Chin,P., Fan,J. and
            Taylor,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-1995) John Taylor, Cardiovascular Disease,
            Gladstone Institute of Cardiovascular Disease, P.O. Box 419100, San
            Francisco, CA 94141-9100, USA
FEATURES             Location/Qualifiers
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     misc_signal     1..774
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                     /note="APOC1 and APOE genes"
                     /function="hepatic control region"
ORIGIN

  Query Match             100.0%;  Score 154;  DB 8;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Db         81 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 140

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db        141 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 200

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db        201 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 234


RESULT 5
AX358722
LOCUS       AX358722               41907 bp    DNA     linear   PAT 13-FEB-2002
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DEFINITION  Sequence 100 from Patent WO0190419.
ACCESSION   AX358722
VERSION     AX358722.1  GI:18675256
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stanton,V.P.
  TITLE     Methods for genetic analysis of dna to detect sequence variances
  JOURNAL   Patent: WO 0190419-A 100 29-NOV-2001;
            Variagenics, Inc. (US) ; Stanton; Vincent P., Jr. (US)
FEATURES             Location/Qualifiers
     source          1. .41907
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             100.0%;  Score 154;  DB 6;  Length 41907;
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  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Db      36908 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 36967

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db      36968 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 37027

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db      37028 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 37061


RESULT 6
AF050154
LOCUS       AF050154                41907 bp    DNA     linear   PRI 10-MAR-1999
DEFINITION  Homo sapiens clone F19374 APO E-C2 gene cluster, complete sequence.
ACCESSION   AF050154 AB012576
VERSION     AF050154.1  GI:4105701
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 41907)
  AUTHORS   Freitas,E.M., Zhang,W.J., Lalonde,J.P., Tay,G.K., Gaudieri,S.,
            Ashworth,L.K., Van Bockxmeer,F.M. and Dawkins,R.L.
  TITLE     Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
            PEREC1
  JOURNAL   DNA Seq. 9 (2), 89-100 (1998)
   PUBMED   10520737
REFERENCE   2  (bases 1 to 41907)
  AUTHORS   Freitas,E.M. and Zhang,W.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-FEB-1998) Centre for Molecular Immunology and
            Instrumentation, University of Western Australia, PO Box 507,
            Subiaco, WA 6008, Australia
REFERENCE   3  (bases 1 to 41907)
  AUTHORS   Dawkins,R.L. and Tay,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-1998) Centre for Molecular Immunology and
            Instrumentation, University of Western Australia, Verdun Street,
            Nedlands, WA 6008, Australia
COMMENT     On Jan 5, 1999 this sequence version replaced gi:3551202.
FEATURES             Location/Qualifiers
     source          1. .41907
                     /organism="Homo sapiens"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-42;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
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Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db      36968 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 37027

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db      37028 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 37061


RESULT 7
AC011481
LOCUS       AC011481               107567 bp    DNA     linear   PRI 29-MAR-2001
DEFINITION  Homo sapiens chromosome 19 clone CTB-129P6, complete sequence.
ACCESSION   AC011481
VERSION     AC011481.4  GI:13487947
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 107567)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 107567)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 107567)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 29, 2001 this sequence version replaced gi:8576069.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.4.
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="CTB-129P6"
ORIGIN

  Query Match             100.0%;  Score 154;  DB 8;  Length 107567;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-42;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67169 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 67228

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67229 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 67288

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      67289 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 67322


RESULT 8
AC021988
LOCUS       AC021988               208239 bp    DNA     linear   HTG 07-JUL-2000
DEFINITION  Homo sapiens chromosome 19 clone RP11-84C16, WORKING DRAFT
            SEQUENCE, 16 unordered pieces.
ACCESSION   AC021988
VERSION     AC021988.4  GI:8569766
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 208239)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 208239)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jun 16, 2000 this sequence version replaced gi:7230864.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0084C16
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 95%
            Sequencing vector: plasmid; 5%
            Chemistry: Dye-primer ET; 95% of reads
            Chemistry: Dye-terminator Big Dye; 5% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 192142 bases at least Q40
            Consensus quality: 197519 bases at least Q30
            Consensus quality: 200851 bases at least Q20
            Insert size: 198000; agarose-fp
            Insert size: 206739; sum-of-contigs
            Quality coverage: 5.02 in Q20 bases; agarose-fp
            Quality coverage: 4.88 in Q20 bases; sum-of-contigs
            -------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
```

```
            * consists of 16 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1607: contig of 1607 bp in length
            *     1608     1707: gap of unknown length
            *     1708     3348: contig of 1641 bp in length
            *     3349     3448: gap of unknown length
            *     3449     5455: contig of 2007 bp in length
            *     5456     5555: gap of unknown length
            *     5556     7647: contig of 2092 bp in length
            *     7648     7747: gap of unknown length
            *     7748    13438: contig of 5691 bp in length
            *    13439    13538: gap of unknown length
            *    13539    22131: contig of 8593 bp in length
            *    22132    22231: gap of unknown length
            *    22232    29647: contig of 7416 bp in length
            *    29648    29747: gap of unknown length
            *    29748    38039: contig of 8292 bp in length
            *    38040    38139: gap of unknown length
            *    38140    46458: contig of 8319 bp in length
            *    46459    46558: gap of unknown length
            *    46559    57985: contig of 11427 bp in length
            *    57986    58085: gap of unknown length
            *    58086    72521: contig of 14436 bp in length
            *    72522    72621: gap of unknown length
            *    72622    88797: contig of 16176 bp in length
            *    88798    88897: gap of unknown length
            *    88898   107698: contig of 18801 bp in length
            *   107699   107798: gap of unknown length
            *   107799   134577: contig of 26779 bp in length
            *   134578   134677: gap of unknown length
            *   134678   163159: contig of 28482 bp in length
            *   163160   163259: gap of unknown length
            *   163260   208239: contig of 44980 bp in length.
FEATURES             Location/Qualifiers
     source          1. .208239
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="RP11-84C16"
     misc_feature    1. .1607
                     /note="assembly_name:Contig13"
     gap             1608. .1707
                     /estimated_length=unknown
     misc_feature    1708. .3348
                     /note="assembly_name:Contig15"
     gap             3349. .3448
                     /estimated_length=unknown
     misc_feature    3449. .5455
                     /note="assembly_name:Contig16"
     gap             5456. .5555
                     /estimated_length=unknown
     misc_feature    5556. .7647
                     /note="assembly_name:Contig17"
     gap             7648. .7747
                     /estimated_length=unknown
     misc_feature    7748. .13438
                     /note="assembly_name:Contig18"
     gap             13439. .13538
                     /estimated_length=unknown
     misc_feature    13539. .22131
                     /note="assembly_name:Contig19"
     gap             22132. .22231
                     /estimated_length=unknown
     misc_feature    22232. .29647
                     /note="assembly_name:Contig20
                     clone_end:T7
                     vector_side:right"
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     gap             29648. .29747
                     /estimated_length=unknown
     misc_feature    29748. .38039
                     /note="assembly_name:Contig21"
     gap             38040. .38139
                     /estimated_length=unknown
     misc_feature    38140. .46458
                     /note="assembly_name:Contig22"
     gap             46459. .46558
                     /estimated_length=unknown
     misc_feature    46559. .57985
                     /note="assembly_name:Contig23"
     gap             57986. .58085
                     /estimated_length=unknown
     misc_feature    58086. .72521
                     /note="assembly_name:Contig24"
     gap             72522. .72621
                     /estimated_length=unknown
     misc_feature    72622. .88797
                     /note="assembly_name:Contig25"
     gap             88798. .88897
                     /estimated_length=unknown
     misc_feature    88898. .107698
                     /note="assembly_name:Contig26"
     gap             107699. .107798
                     /estimated_length=unknown
     misc_feature    107799. .134577
                     /note="assembly_name:Contig27"
     gap             134578. .134677
                     /estimated_length=unknown
     misc_feature    134678. .163159
                     /note="assembly_name:Contig28"
     gap             163160. .163259
                     /estimated_length=unknown
     misc_feature    163260. .208239
                     /note="assembly_name:Contig29"
ORIGIN

  Query Match             92.2%;  Score 142;  DB 14;  Length 208239;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-38;
  Matches  153;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26104 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 26163

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26164 ATGGGC-AACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 26222

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      26223 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 26256


RESULT 9
AC146473
LOCUS       AC146473               39483 bp    DNA     linear   HTG 16-AUG-2003
DEFINITION  Hylobates klossii clone RZ140-83M19, WORKING DRAFT SEQUENCE, 2
            ordered pieces.
ACCESSION   AC146473
VERSION     AC146473.1  GI:33695020
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Hylobates klossii (Kloss's gibbon)
  ORGANISM  Hylobates klossii
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hylobatidae; Hylobates.
REFERENCE   1  (bases 1 to 39483)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
```

```
REFERENCE   2  (bases 1 to 39483)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT
            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: I005
            Bac Clone Name: RZ140-83M19

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    22109: contig of 22109 bp in length
            *    22110    22209: gap of unknown length
            *    22210    39483: contig of 17274 bp in length.
FEATURES             Location/Qualifiers
     source          1. .39483
                     /organism="Hylobates klossii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9587"
                     /clone="RZ140-83M19"
     gap             22110. .22209
                     /estimated_length=unknown
ORIGIN

  Query Match             91.7%;  Score 141.2;  DB 14;  Length 39483;
  Best Local Similarity   94.8%;  Pred. No. 3.8e-38;
  Matches  146;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||| |||||||| ||||||||| ||| ||||||||||
Db      31854 GTTTGTGTGCTGCCTCTGAAGTCCACCCTGAACAACCTTCAGCCTGCTCCTGTCCCTAAA 31913

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||| |
Db      31914 ATGGGCAAACATTGCAAGAAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCCT 31973

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              |||||||||||||||||||| |||||| ||||||
Db      31974 GGAGCTGGGGCAGAGGTCAGGGACCTCCCTGGGC 32007


RESULT 10
AC145523
LOCUS       AC145523              183798 bp    DNA     linear   HTG 05-AUG-2003
DEFINITION  Papio hamadryas clone RP41-112M21, WORKING DRAFT SEQUENCE, 4
            ordered pieces.
ACCESSION   AC145523
VERSION     AC145523.2  GI:33438604
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio hamadryas (hamadryas baboon)
  ORGANISM  Papio hamadryas
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
REFERENCE   3  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT     On Aug 5, 2003 this sequence version replaced gi:32996764.

            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: B056
            Bac Clone Name: RP41-112M21

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    59944: contig of 59944 bp in length
            *    59945    60044: gap of unknown length
            *    60045   168286: contig of 108242 bp in length
            *   168287   168386: gap of unknown length
            *   168387   171995: contig of 3609 bp in length
            *   171996   172095: gap of unknown length
            *   172096   183798: contig of 11703 bp in length.
FEATURES             Location/Qualifiers
     source          1. .183798
                     /organism="Papio hamadryas"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9557"
                     /clone="RP41-112M21"
     gap             59945. .60044
                     /estimated_length=unknown
```

```
     gap             168287. .168386
                     /estimated_length=unknown
     gap             171996. .172095
                     /estimated_length=unknown
ORIGIN

  Query Match             90.6%;  Score 139.6;  DB 14;  Length 183798;
  Best Local Similarity   94.2%;  Pred. No. 1.8e-37;
  Matches  145;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||  |||||||| |||||||||  ||  |||||||||
Db     162213 GTTTGTGTGCTGCCTCTGAAGTCCAGCCTGAACAACCTTCAGCCTGTTCCCGTCCCTAAA 162272

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     162273 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCGTGCTGACCTT 162332

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||| ||||||
Db     162333 GGAGCTGGGGCAGAGGTCAGAGACCTCCCTGGGC 162366


RESULT 11
AC148222
LOCUS       AC148222               231234 bp    DNA     linear   HTG 14-FEB-2004
DEFINITION  Colobus guereza clone CH272-38C16, WORKING DRAFT SEQUENCE, 8
            ordered pieces.
ACCESSION   AC148222
VERSION     AC148222.1  GI:42557404
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Colobus guereza (guereza)
  ORGANISM  Colobus guereza
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Colobinae; Colobus.
REFERENCE   1  (bases 1 to 231234)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 231234)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-FEB-2004) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT
            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: CL013
            Bac Clone Name: CH272-38C16

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *          1     69606: contig of 69606 bp in length
            *      69607     69706: gap of unknown length
            *      69707     78173: contig of 8467 bp in length
            *      78174     78273: gap of unknown length
            *      78274    110638: contig of 32365 bp in length
            *     110639    110738: gap of unknown length
            *     110739    117542: contig of 6804 bp in length
            *     117543    117642: gap of unknown length
            *     117643    121544: contig of 3902 bp in length
            *     121545    121644: gap of unknown length
            *     121645    163598: contig of 41954 bp in length
            *     163599    163698: gap of unknown length
            *     163699    199977: contig of 36279 bp in length
            *     199978    200077: gap of unknown length
            *     200078    231234: contig of 31157 bp in length.
FEATURES             Location/Qualifiers
     source          1. .231234
                     /organism="Colobus guereza"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:33548"
                     /clone="CH272-38C16"
     gap             69607. .69706
                     /estimated_length=unknown
     gap             78174. .78273
                     /estimated_length=unknown
     gap             110639. .110738
                     /estimated_length=unknown
     gap             117543. .117642
                     /estimated_length=unknown
     gap             121545. .121644
                     /estimated_length=unknown
     gap             163599. .163698
                     /estimated_length=unknown
     gap             199978. .200077
                     /estimated_length=unknown
ORIGIN

  Query Match             88.6%;  Score 136.4;  DB 14;  Length 231234;
  Best Local Similarity   92.9%;  Pred. No. 2.5e-36;
  Matches  143;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||  |||||||| ||||| ||| ||| ||||||||||
Db     178100 GTTTGTGTGCTGCCTCTGAAGTCCAGCCTGAACAACCTTCATCCTGCTCCTGTCCCTAAA 178159

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              |||||||||||||||||||||| ||||||||||| |||||||||||||| ||||||||||
Db     178160 ATGGGCAAACATTGCAAGCAGCCAACAGCAAACATACAGCCCTCCCTGCGTGCTGACCTT 178219

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||| ||||||||||||||||||||||| ||||||
Db     178220 GGAACTGGGGCAGAGGTCAGAGACCTCCCTGGGC 178253


RESULT 12
HSU35114
LOCUS       HSU35114                 4097 bp    DNA     linear   PRI 07-NOV-1996
DEFINITION  Human apolipoprotein E (APOE) gene, hepatic control region HCR-2.
ACCESSION   U35114
VERSION     U35114.1  GI:1049244
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4097)
```

```
  AUTHORS   Dang,Q. and Taylor,J.
  TITLE     In vivo footprinting analysis of the hepatic control region of the
            human apolipoprotein E/C-I/C-IV/C-II gene locus
  JOURNAL   J. Biol. Chem. 271 (45), 28667-28676 (1996)
   PUBMED   8910501
REFERENCE   2  (bases 1 to 4097)
  AUTHORS   Allan,C.M., Walker,D. and Taylor,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-AUG-1995) John Taylor, Cardiovascular, Gladstone
            Institute, P.O. Box 419100, San Francisco, CA 94141-9100, USA
FEATURES             Location/Qualifiers
     source          1. .4097
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="DNA sequenced was from a P1 plasmid clone from a
                     human genomic library from Genome Systems, Inc., St.
                     Louis, MO;chromosome 19q"
     gene            1. .4097
                     /gene="APOE"
     misc_signal     1. .4097
                     /gene="APOE"
                     /standard_name="HCR-2"
                     /function="hepatic control region"
ORIGIN

  Query Match            85.5%;  Score 131.6;  DB 8;  Length 4097;
  Best Local Similarity  90.9%;  Pred. No. 6.7e-35;
  Matches  140;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||| |||||   | |||||||||  ||  |||||| | 
Db        132 GTTTGTGTGCTGCCTCTGAAGTCCACCCTGAATGACCTTCAGCCTGTTCCCGTCCCTGAT 191

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              |||||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        192 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACATAGCCCTCCCTGCGTGCTGACCTT 251

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||| ||||||||||||||||||||| ||||
Db        252 GGAGCTGCGGCAGAGGTCAGAGACCTCTCAGGGC 285


RESULT 13
AC120211/c
LOCUS       AC120211               63931 bp    DNA     linear   HTG 04-MAY-2002
DEFINITION  Pan troglodytes clone RP43-174J24, WORKING DRAFT SEQUENCE, 20
            unordered pieces.
ACCESSION   AC120211
VERSION     AC120211.1  GI:20451083
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 63931)
  AUTHORS   Martin,J., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and
            Cheng,J.-F.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 63931)
  AUTHORS   Martin,J., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and
            Cheng,J.-F.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2002) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT     Draft Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Additional information:
            Comparative analysis and ordering by homology are available
            here: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOE
```

```
            Funding agent: Programs for Genomic Applications (NHLBI)
            Contact: 'Jody Schwartz' jrschwartz@lbl.gov
            Summary Statistics
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *          1     2246: contig of 2246 bp in length
            *       2247     2346: gap of unknown length
            *       2347     4620: contig of 2274 bp in length
            *       4621     4720: gap of unknown length
            *       4721     6912: contig of 2192 bp in length
            *       6913     7012: gap of unknown length
            *       7013     9135: contig of 2123 bp in length
            *       9136     9235: gap of unknown length
            *       9236    11899: contig of 2664 bp in length
            *      11900    11999: gap of unknown length
            *      12000    14152: contig of 2153 bp in length
            *      14153    14252: gap of unknown length
            *      14253    17633: contig of 3381 bp in length
            *      17634    17733: gap of unknown length
            *      17734    21051: contig of 3318 bp in length
            *      21052    21151: gap of unknown length
            *      21152    25022: contig of 3871 bp in length
            *      25023    25122: gap of unknown length
            *      25123    27204: contig of 2082 bp in length
            *      27205    27304: gap of unknown length
            *      27305    29686: contig of 2382 bp in length
            *      29687    29786: gap of unknown length
            *      29787    31937: contig of 2151 bp in length
            *      31938    32037: gap of unknown length
            *      32038    34727: contig of 2690 bp in length
            *      34728    34827: gap of unknown length
            *      34828    38304: contig of 3477 bp in length
            *      38305    38404: gap of unknown length
            *      38405    42265: contig of 3861 bp in length
            *      42266    42365: gap of unknown length
            *      42366    45543: contig of 3178 bp in length
            *      45544    45643: gap of unknown length
            *      45644    49570: contig of 3927 bp in length
            *      49571    49670: gap of unknown length
            *      49671    53133: contig of 3463 bp in length
            *      53134    53233: gap of unknown length
            *      53234    60427: contig of 7194 bp in length
            *      60428    60527: gap of unknown length
            *      60528    63931: contig of 3404 bp in length.
FEATURES             Location/Qualifiers
     source          1. .63931
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-174J24"
     gap             2247. .2346
                     /estimated_length=unknown
     gap             4621. .4720
                     /estimated_length=unknown
     gap             6913. .7012
                     /estimated_length=unknown
     gap             9136. .9235
                     /estimated_length=unknown
     gap             11900. .11999
                     /estimated_length=unknown
     gap             14153. .14252
                     /estimated_length=unknown
     gap             17634. .17733
                     /estimated_length=unknown
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     gap             21052. .21151
                     /estimated_length=unknown
     gap             25023. .25122
                     /estimated_length=unknown
     gap             27205. .27304
                     /estimated_length=unknown
     gap             29687. .29786
                     /estimated_length=unknown
     gap             31938. .32037
                     /estimated_length=unknown
     gap             34728. .34827
                     /estimated_length=unknown
     gap             38305. .38404
                     /estimated_length=unknown
     gap             42266. .42365
                     /estimated_length=unknown
     gap             45544. .45643
                     /estimated_length=unknown
     gap             49571. .49670
                     /estimated_length=unknown
     gap             53134. .53233
                     /estimated_length=unknown
     gap             60428. .60527
                     /estimated_length=unknown
ORIGIN

  Query Match             85.5%;  Score 131.6;  DB 14;  Length 63931;
  Best Local Similarity   90.9%;  Pred. No. 1e-34;
  Matches  140;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||| |||||  | |||||||||  ||  |||||| |
Db       3331 GTTTGTGTGCTGCCTCTGAAGTCCACCCTGAATGACCTTCAGCCTGTTCCCGTCCCTGAG 3272

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              |||||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db       3271 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACATAGCCCTCCCTGCGTGCTGACCTT 3212

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||| ||||||||||||||||||||| ||||
Db       3211 GGAGCTGCGGCAGAGGTCAGAGACCTCTCAGGGC 3178


RESULT 14
AC145523/c
LOCUS       AC145523              183798 bp    DNA     linear   HTG 05-AUG-2003
DEFINITION  Papio hamadryas clone RP41-112M21, WORKING DRAFT SEQUENCE, 4
            ordered pieces.
ACCESSION   AC145523
VERSION     AC145523.2  GI:33438604
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio hamadryas (hamadryas baboon)
  ORGANISM  Papio hamadryas
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
REFERENCE   3  (bases 1 to 183798)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT     On Aug 5, 2003 this sequence version replaced gi:32996764.

            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: B056
            Bac Clone Name: RP41-112M21

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1     59944: contig of 59944 bp in length
            *    59945     60044: gap of unknown length
            *    60045    168286: contig of 108242 bp in length
            *   168287    168386: gap of unknown length
            *   168387    171995: contig of 3609 bp in length
            *   171996    172095: gap of unknown length
            *   172096    183798: contig of 11703 bp in length.
FEATURES             Location/Qualifiers
     source          1. .183798
                     /organism="Papio hamadryas"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9557"
                     /clone="RP41-112M21"
     gap             59945. .60044
                     /estimated_length=unknown
     gap             168287. .168386
                     /estimated_length=unknown
     gap             171996. .172095
                     /estimated_length=unknown
ORIGIN

  Query Match             84.4%;  Score 130;  DB 14;  Length 183798;
  Best Local Similarity   90.3%;  Pred. No. 4.4e-34;
  Matches  139;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              |||||||||||||||||||||||||  |||||  | |||||||||  ||  |||||| |
Db      67062 GTTTGTGTGCTGCCTCTGAAGTCCAGCCTGAATGACCTTCAGCCTGTTCCCGTCCCTGAG 67003

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db      67002 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGTGTGCTGACCTT 66943

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||| ||||||||||||||||||||||| ||||||
Db      66942 GGAACTGGGGCAGAGGTCAGAGACCTCCCTGGGC 66909


RESULT 15
AC146285
```

```
LOCUS       AC146285               185724 bp    DNA     linear   HTG 07-AUG-2003
DEFINITION  Callicebus moloch clone LB5-404K13, WORKING DRAFT SEQUENCE, 6
            ordered pieces.
ACCESSION   AC146285
VERSION     AC146285.2  GI:33469171
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Callicebus moloch (Dusky titi)
  ORGANISM  Callicebus moloch
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
            Cebidae; Callicebinae; Callicebus.
REFERENCE   1  (bases 1 to 185724)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 185724)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
REFERENCE   3  (bases 1 to 185724)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT     On Aug 7, 2003 this sequence version replaced gi:33413350.

            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: T019
            Bac Clone Name: LB5-404K13

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            If the Bac Library Name is LB1 to LB4, please see website
            for the description: http://www-gsd.lbl.gov/cheng/BAC.html
            These libraries are available through the BACPAC Resources Center:
            http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1     6536: contig of 6536 bp in length
            *     6537     6636: gap of unknown length
            *     6637    54159: contig of 47523 bp in length
            *    54160    54259: gap of unknown length
            *    54260    76479: contig of 22220 bp in length
            *    76480    76579: gap of unknown length
            *    76580   110159: contig of 33580 bp in length
            *   110160   110259: gap of unknown length
            *   110260   133023: contig of 22764 bp in length
            *   133024   133123: gap of unknown length
            *   133124   185724: contig of 52601 bp in length.
FEATURES             Location/Qualifiers
     source          1..185724
                     /organism="Callicebus moloch"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9523"
                     /clone="LB5-404K13"
     gap             6537..6636
                     /estimated_length=unknown
     gap             54160..54259
                     /estimated_length=unknown
     gap             76480..76579
                     /estimated_length=unknown
     gap             110160..110259
                     /estimated_length=unknown
     gap             133024..133123
                     /estimated_length=unknown
ORIGIN

  Query Match             74.3%;  Score 114.4;  DB 14;  Length 185724;
  Best Local Similarity   87.3%;  Pred. No. 1.4e-28;
  Matches  138;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    1;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||| |||||||||||||||||||| |||||| | |||||||||  || ||||||| |
Db     148042 GTTTGCGTGCTGCCTCTGAAGTCCACCCTGAACGACCTTCAGCCTGTTCCTGTCCCTGAG 148101

Qy         61 ATGGGCAAACATTGCAAG----CAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              ||||||||||||||||||    ||||||||||||||||| ||||||| ||||| ||||||
Db     148102 ATGGGCAAACATTGCAAGCAAACAGCAAACAGCAAACACGCAGCCCTGCCTGCGTGCTGA 148161

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||| ||||||||||||||||||||||||||| | || |
Db     148162 CCTGGGAGCTGGGGCAGAGGTCAGAGACCTCCCGGGCC 148199


Search completed: April 18, 2006, 14:56:52
Job time : 848.062 secs
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                 GenCore version 5.1.7
         Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:03:10 ; Search time 93.4261 Seconds
                                           (without alignments)
                                           10985.822 Million cell updates/sec

Title:          US-09-884-901A-8
Perfect score:  154
Sequence:       1 gtttgtgtgctgcctctgaa..........ggtcagagacctctctgggc 154

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:      9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_21:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                   %
Result          Query
  No.   Score   Match Length DB  ID                      Description
 ------------------------------------------------------------------------
     1    154   100.0    154  6  AAI71009                Aai71009 Human apo
     2    154   100.0    328  6  AAI71010                Aai71010 Human apo
     3    154   100.0    771  6  AAI71005                Aai71005 Human apo
     4    154   100.0    774  2  AAQ92616                Aaq92616 Human hep
     5    154   100.0   1079  6  ABL31916                Abl31916 Human Apo
     6    151    98.1    154  6  ABV73262                Abv73262 Apolipopr
     7     82    53.2     90  2  AAV19597                Aav19597 Apolipopr
     8     82    53.2     90  2  AAV19593                Aav19593 Apolipopr
     9     82    53.2     90  2  AAV15382                Aav15382 ApoE enha
    10     82    53.2     90  2  AAV15386                Aav15386 ApoE enha
    11     82    53.2     90 13   ADU47587                Adu47587 Oligonucl
    12     82    53.2     90 13   ADU47583                Adu47583 Oligonucl
c   13     78    50.6     82  2  AAV19599                Aav19599 Apolipopr
c   14     78    50.6     82 13   ADU47589                Adu47589 Oligonucl
c   15     77    50.0     82  2  AAV19595                Aav19595 Apolipopr
c   16     77    50.0     82 13   ADU47585                Adu47585 Oligonucl
c   17   76.4    49.6     82  2  AAV15388                Aav15388 ApoE enha
c   18   75.4    49.0     82  2  AAV15384                Aav15384 ApoE enha
c   19     74    48.1     78  2  AAV19596                Aav19596 Apolipopr
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c   20     74    48.1     78  2  AAV19600                Aav19600 Apolipopr
c   21     74    48.1     78  2  AAV15385                Aav15385 ApoE enha
c   22     74    48.1     78 13   ADU47590                Adu47590 Oligonucl
c   23     74    48.1     78 13   ADU47586                Adu47586 Oligonucl
c   24   72.4    47.0     78  2  AAV15389                Aav15389 ApoE enha
    25     70    45.5     70  2  AAV19598                Aav19598 Apolipopr
    26     70    45.5     70  2  AAV15387                Aav15387 ApoE enha
    27     70    45.5     70 13   ADU47588                Adu47588 Oligonucl
    28     69    44.8     70  2  AAV19594                Aav19594 Apolipopr
    29     69    44.8     70  2  AAV15383                Aav15383 ApoE enha
    30     69    44.8     70 13   ADU47584                Adu47584 Oligonucl
c   31     32    20.8   2235 11   ACL27536                Acl27536 Rice abio
c   32   31.6    20.5   1179 10   ADG73621                Adg73621 Human cDN
c   33   31.4    20.4  88191  8  ABX14763                Abx14763 Genomic D
    34   31.2    20.3    257  4  ABA75079                Aba75079 Human foe
    35   31.2    20.3    257  4  AAI55613                Aai55613 Probe #24
    36   31.2    20.3    257  4  ABA39763                Aba39763 Probe #18
    37   31.2    20.3    257  4  AAK49722                Aak49722 Human bon
    38   31.2    20.3    257  4  AAK23594                Aak23594 Human bra
    39   31.2    20.3    257  4  ABS49348                Abs49348 Human liv
    40   31.2    20.3    257  6  ABS23212                Abs23212 Human gen
    41   31.2    20.3    567  4  ABA62558                Aba62558 Human foe
    42   31.2    20.3    567  4  AAI42544                Aai42544 Probe #11
    43   31.2    20.3    567  4  ABA29886                Aba29886 Probe #83
    44   31.2    20.3    567  4  AAK36772                Aak36772 Human bon
    45   31.2    20.3    567  4  AAK10914                Aak10914 Human bra

                                ALIGNMENTS


RESULT 1
AAI71009
ID   AAI71009 standard; DNA; 154 BP.
XX
AC   AAI71009;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human apolipoprotein E gene enhancer.
XX
KW   Apolipoprotein E; ApoE; enhancer; human; expression cassette; liver;
KW   Factor IX; blood clotting; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200198482-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-US019634.
XX
PR   20-JUN-2000; 2000US-0212902P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Miao CH,  Kay MA;
XX
DR   WPI; 2002-114582/15.
XX
PT   Nucleic acid construct for expressing nucleic acid molecules, proteins in
PT   mammalian liver cells, has operably linked hepatic locus control element,
PT   hepatic promoter, coding sequence, polyadenylation signal and intron.
XX
PS   Example 2; Page 59; 64pp; English.
XX
CC   The present sequence is that of an enhancer sequence from the human
CC   apolipoprotein E gene. The enhancer may be incorporated into expression
CC   cassettes of the invention designed for liver-specific expression of
CC   Factor IX. The cassettes also include an hepatic locus control region
CC   located 5' to a liver-specific promoter, a Factor IX coding sequence, a
CC   3' polyadenylation signal, and an intron (see AAI71003-16). Also provided
```

```
CC   are vectors that include an expression cassette of the invention. These
CC   may episomal or integrating vectors, including viral vectors, and are
CC   used in a claimed method of ameliorating the symptoms of a disease. A
CC   therapeutic amount of blood clotting Factor IX is produced in mammalian
CC   liver cells for at least 100, and preferably at least 500, days. In
CC   examples of the invention, human Factor IX was expressed in mouse liver
CC   cells following injection of retrovirus-based plasmids that carried the
CC   expression cassettes into the tail vein or portal vein, and by direct
CC   injection of plasmid DNA into the liver
XX
SQ   Sequence 154 BP; 40 A; 47 C; 36 G; 31 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 154;  DB 6;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-40;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154


RESULT 2
AAI71010
ID   AAI71010 standard; DNA; 328 BP.
XX
AC   AAI71010;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human apolipoprotein E gene hepatic locus control element.
XX
KW   Apolipoprotein E; ApoE; hepatic locus control element; human;
KW   expression cassette; liver; Factor IX; blood clotting; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200198482-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-US019634.
XX
PR   20-JUN-2000; 2000US-0212902P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Miao CH,  Kay MA;
XX
DR   WPI; 2002-114582/15.
XX
PT   Nucleic acid construct for expressing nucleic acid molecules, proteins in
PT   mammalian liver cells, has operably linked hepatic locus control element,
PT   hepatic promoter, coding sequence, polyadenylation signal and intron.
XX
PS   Example 2; Page 59; 64pp; English.
XX
CC   The present sequence is that of the hepatic locus control element of the
CC   human apolipoprotein E gene. The sequence can be incorporated into
CC   expression cassettes of the invention designed for liver-specific
CC   expression of Factor IX. The cassettes also include an hepatic promoter
CC   located 3' to the hepatic locus control element, the Factor IX coding
CC   sequence, a 3' polyadenylation signal, and an intron located 3' to the
CC   hepatic promoter and 5' to the polyadenylation signal (see AAI71003-16).
CC   The hepatic locus control element confers copy number dependent, position
```

```
CC   independent gene expression. Also provided are vectors that include an
CC   expression cassette of the invention. These may episomal or integrating
CC   vectors, including viral vectors. They are used in a claimed method of
CC   ameliorating the symptoms of a disease. A therapeutic amount of blood
CC   clotting Factor IX is produced in mammalian liver cells for a period of
CC   at least 100 days, and preferably at least 500 days. In examples of the
CC   invention, human Factor IX was expressed in mouse liver cells following
CC   injection of retrovirus-based plasmids carrying the expression cassettes
CC   into the tail vein or portal vein, and by direct injection of plasmid DNA
CC   into the liver
XX
SQ   Sequence 328 BP; 72 A; 104 C; 84 G; 68 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 154;  DB 6;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-40;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 137

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 197

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        198 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 231


RESULT 3
AAI71005
ID   AAI71005 standard; DNA; 771 BP.
XX
AC   AAI71005;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human apolipoprotein E ApoE-HCR gene hepatic locus control element.
XX
KW   Apolipoprotein E; ApoE-HCR; hepatic locus control element; human;
KW   expression cassette; liver; Factor IX; blood clotting; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200198482-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-US019634.
XX
PR   20-JUN-2000; 2000US-0212902P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Miao CH,  Kay MA;
XX
DR   WPI; 2002-114582/15.
XX
PT   Nucleic acid construct for expressing nucleic acid molecules, proteins in
PT   mammalian liver cells, has operably linked hepatic locus control element,
PT   hepatic promoter, coding sequence, polyadenylation signal and intron.
XX
PS   Claim 7; Page 56-57; 64pp; English.
XX
CC   The present sequence is that of the hepatic locus control element of the
CC   human apolipoprotein E gene, ApoE-HCR. The sequence can be incorporated
CC   into expression cassettes of the invention designed for liver-specific
CC   expression of Factor IX. The cassettes also include an hepatic promoter
CC   located 3' to the hepatic locus control element, the Factor IX coding
CC   sequence, a 3' polyadenylation signal, and an intron located 3' to the
CC   hepatic promoter and 5' to the polyadenylation signal (see AAI71003-16).
```

```
CC   The hepatic locus control element confers copy number dependent, position
CC   independent gene expression. Also provided are vectors that include an
CC   expression cassette of the invention. These may episomal or integrating
CC   vectors, including viral vectors. They are used in a claimed method of
CC   ameliorating the symptoms of a disease. A therapeutic amount of blood
CC   clotting Factor IX is produced in mammalian liver cells for a period of
CC   at least 100 days, and preferably at least 500 days. In examples of the
CC   invention, human Factor IX was expressed in mouse liver cells following
CC   injection of retrovirus-based plasmids carrying the expression cassettes
CC   into the tail vein or portal vein, and by direct injection of plasmid DNA
CC   into the liver
XX
SQ   Sequence 771 BP; 165 A; 215 C; 186 G; 205 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 154;  DB 6;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-39;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 137

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 197

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        198 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 231


RESULT 4
AAQ92616
ID   AAQ92616 standard; DNA; 774 BP.
XX
AC   AAQ92616;
XX
DT   19-DEC-1995  (first entry)
XX
DE   Human hepatocyte-specific control region.
XX
KW   Human hepatocyte-specific control region; human afamin; HCR enhancer;
KW   promoter; transgene; transgenic animal;
KW   in vivo system for disease analysis; liver expression; ds.
XX
OS   Homo sapiens.
XX
PN   WO9511308-A1.
XX
PD   27-APR-1995.
XX
PF   13-OCT-1994;   94WO-US011675.
XX
PR   18-OCT-1993;   93US-00141322.
PR   31-MAR-1994;   94US-00221767.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Simonet WS,  Lichenstein HS,  Lyons DE;
XX
DR   WPI; 1995-170228/22.
XX
PT   Nucleic acid sequence for liver specific expression of a trans:gene -
PT   comprises hepatocyte specific control region linked to a promoter and the
PT   trans:gene, and is used for the prodn. of a transgenic mammal.
XX
PS   Claim 1; Fig 1; 73pp; English.
XX
CC   AAQ92616 is the human hepatocyte-specific control region (HCR enhancer),
CC   which was operably linked to a promoter and a transgene, i.e. AAQ92617
CC   which encodes AAR75655, human afamin. The resultant sequence can then be
CC   used in the construction of a transgenic mammal, which can produce
CC   recombinant afamin, the expression of which may be specific to the liver
CC   of the mammal. The mammal may be used as an in vivo system to analyse the
CC   course of a disease
XX
SQ   Sequence 774 BP; 165 A; 214 C; 189 G; 206 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 154;  DB 2;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-39;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 140

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 200

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        201 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 234


RESULT 5
ABL31916
ID   ABL31916 standard; DNA; 1079 BP.
XX
AC   ABL31916;
XX
DT   22-MAR-2002  (first entry)
XX
DE   Human ApoE genomic partial sequence (36601 to 37680).
XX
KW   Genetic analysis; sequence variant detection; genotype; ApoE; SNP;
KW   single nucleotide polymorphism; polymorphic site; atherosclerosis;
KW   dementia; Parkinson's disease; Huntington's disease; PCR primer;
KW   neurodegenerative disease; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200190419-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016577.
XX
PR   23-MAY-2000; 2000US-0206613P.
PR   25-OCT-2000; 2000US-00696998.
PR   25-OCT-2000; 2000US-00697013.
PR   25-OCT-2000; 2000US-00697028.
XX
PA   (VARI-) VARIAGENICS INC.
PA   (STAN/) STANTON V P.
XX
PI   Stanton VP;
XX
DR   WPI; 2002-097670/13.
XX
PT   Determining the haplotype of at least one allele of a selected gene at
PT   two or more polymorphic sites, for assessing disease risk, comprises
PT   allele-specific enrichment, optical mapping, or atomic force microscopy.
XX
PS   Disclosure; Page 103; 166pp; English.
XX
CC   The present invention describes a method for determining the haplotype of
CC   an allele of a selected gene at two or more polymorphic sites comprising
CC   allele-specific enrichment, optical mapping, or atomic force microscopy.
CC   The method is useful for genetic analysis when the DNA segment being
CC   haplotyped consists of polymorphisms that are in some degree of linkage
CC   disequilibrium with each other, that is they do not assort randomly in
CC   the population being studied. The method allows early implementation of
CC   preventive measures in patients at risk of diseases such as
CC   atherosclerosis, dementia, Parkinson's disease, Huntington's disease or
CC   other organic or vascular neurodegenerative diseases. Genotype and
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CC   haplotype information can be used to make diagnostic tests useful for
CC   disease risk assessment, for prognostic prediction of the course or
CC   outcome of a disease, to diagnose a disease or condition, or to select an
CC   optimal therapy for a disease or condition. ABL31915 to ABL32035
CC   represent nucleotide sequence used in the exemplification of the present
CC   invention
XX
SQ   Sequence 1079 BP; 247 A; 284 C; 286 G; 262 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 154;  DB 6;  Length 1079;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-39;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 367

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 427

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db        428 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 461


RESULT 6
ABV73262
ID   ABV73262 standard; DNA; 154 BP.
XX
AC   ABV73262;
XX
DT   22-JAN-2003  (first entry)
XX
DE   Apolipoprotein E locus control region nucleotide sequence.
XX
KW   Adeno-associated virus; AAV; virion; helper virus; secretory gland;
KW   transduction; haemostatic; gene therapy; blood coagulation; haemophilia;
KW   gene transfer; apolipoprotein E; ApoE; ds.
XX
OS   Unidentified.
XX
PN   WO200271843-A1.
XX
PD   19-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-US008350.
XX
PR   14-MAR-2001; 2001US-0275908P.
XX
PA   (AVIG-) AVIGEN INC.
XX
PI   Mcclelland A,  Scolley R;
XX
DR   WPI; 2002-698779/75.
XX
PT   Delivering a protein to a mammal, useful in gene transfer, comprises
PT   contacting recombinant adeno-associated virus virions free of helper
PT   virus and having heterologous gene encoding a protein, with a duct of a
PT   secretory gland of mammal.
XX
PS   Example 1; Page 32; 48pp; English.
XX
CC   The invention relates to delivering a protein to a mammal that involves
CC   contacting recombinant adeno-associated virus (rAAV) virions, which are
CC   free of helper virus, and comprises heterologous gene encoding a protein,
CC   with a duct of a secretory gland of mammal resulting in the transduction
CC   of at least one cell of the secretory gland. The rAAV virion comprising a
CC   heterologous gene is useful in the manufacture of a medicament for
CC   delivery to a duct of a salivary gland, secretory gland or liver of a
CC   mammal. The rAAV virion comprising a gene encoding a blood coagulation
CC   protein may also be used in the manufacture of a medicament for treating
CC   haemophilia. The method is useful in gene transfer, and to facilitate
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CC   pharmaco- or toxico-kinetic studies. The present sequence represents an
CC   apolipoprotein E (ApoE) locus control region nucleotide sequence
XX
SQ   Sequence 154 BP; 40 A; 47 C; 35 G; 32 T; 0 U; 0 Other;

  Query Match             98.1%;  Score 151;  DB 6;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-39;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 63

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 123

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
              |||||||||||||||||||||||||||||||
Db        124 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 154


RESULT 7
AAV19597
ID   AAV19597 standard; DNA; 90 BP.
XX
AC   AAV19597;
XX
DT   25-MAR-2003  (revised)
DT   06-AUG-1998  (first entry)
XX
DE   Apolipoprotein E (Apo E) enhancer sequence generating sense primer 3.
XX
KW   Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW   haemophilia; thrombosis; hypercoagulable disorder; liver disease;
KW   hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human;
KW   cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi;
KW   diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection;
KW   anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;
KW   autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E;
KW   enhancer sequence; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800541-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011784.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Barber JR,  Chang SMW,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J,  Lee R;
XX
DR   WPI; 1998-086966/08.
XX
PT   New replication defective recombinant retro-viruses - which can be
PT   administered to provide long term systemic expression of therapeutic
PT   protein in blood, useful in, e.g. treating hyper-coagulable disorders.
XX
PS   Example 33; Page 178; 272pp; English.
XX
CC   This primer is used for generating the apolipoprotein E (Apo E) enhancer
CC   sequence. This is used to construct a retroviral vector backbone with a
CC   liver specific promoter. The invention provides the preparation of
CC   replication defective recombinant retrovirus (RRV) expressing a
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CC   therapeutic protein. The RRV preparation is resistant to degradation by
CC   human complement and is capable of inducing long term systemic expression
CC   of the therapeutic protein when administered intravenously to a human.
CC   The long term systemic expression results in a measurable level of the
CC   therapeutic protein being produced in the blood of the human for a period
CC   of at least 30 days after the administration of the RRV vector
CC   preparation. The RRV's can be used for in vivo delivery of therapeutic
CC   protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
CC   hypercoagulable disorders, liver diseases such as hepatitis, disorders
CC   such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
CC   combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular
CC   Dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
CC   hypopituitarism, adenine deaminase deficiency, alpha1-antitrypsin
CC   deficiency, Guacher's syndrome, anaemia, infections such as HIV
CC   infection, high blood pressure, Alzheimer's disease, autoimmune or
CC   inflammatory disease or graft versus host disease. RRV's are capable of
CC   surviving inactivation in human serum thereby allowing efficient gene
CC   transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 8
AAV19593
ID   AAV19593 standard; DNA; 90 BP.
XX
AC   AAV19593;
XX
DT   25-MAR-2003  (revised)
DT   06-AUG-1998  (first entry)
XX
DE   Apolipoprotein E (Apo E) enhancer sequence generating sense primer 1.
XX
KW   Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW   haemophilia; thrombosis; hypercoagulable disorder; liver disease;
KW   hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human;
KW   cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi;
KW   diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection;
KW   anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;
KW   autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E;
KW   enhancer sequence; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800541-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011784.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Barber JR,  Chang SMW,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J,  Lee R;
```

```
XX
DR   WPI; 1998-086966/08.
XX
PT   New replication defective recombinant retro-viruses - which can be
PT   administered to provide long term systemic expression of therapeutic
PT   protein in blood, useful in, e.g. treating hyper-coagulable disorders.
XX
PS   Example 33; Page 177; 272pp; English.
XX
CC   This primer is used for generating the apolipoprotein E (Apo E) enhancer
CC   sequence. This is used to construct a retroviral vector backbone with a
CC   liver specific promoter. The invention provides the preparation of
CC   replication defective recombinant retrovirus (RRV) expressing a
CC   therapeutic protein. The RRV preparation is resistant to degradation by
CC   human complement and is capable of inducing long term systemic expression
CC   of the therapeutic protein when administered intravenously to a human.
CC   The long term systemic expression results in a measurable level of the
CC   therapeutic protein being produced in the blood of the human for a period
CC   of at least 30 days after the administration of the RRV vector
CC   preparation. The RRV's can be used for in vivo delivery of therapeutic
CC   protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
CC   hypercoagulable disorders, liver diseases such as hepatitis, disorders
CC   such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
CC   combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular
CC   Dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
CC   hypopituitarism, adenine deaminase deficiency, alpha1-antitrypsin
CC   deficiency, Guacher's syndrome, anaemia, infections such as HIV
CC   infection, high blood pressure, Alzheimer's disease, autoimmune or
CC   inflammatory disease or graft versus host disease. RRV's are capable of
CC   surviving inactivation in human serum thereby allowing efficient gene
CC   transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 9
AAV15382
ID   AAV15382 standard; DNA; 90 BP.
XX
AC   AAV15382;
XX
DT   20-JUL-1998  (first entry)
XX
DE   ApoE enhancer sense oligonucleotide.
XX
KW   Gene therapy; retrovirus; vector; apolipoprotein E; ApoE; enhancer;
KW   human; interferon; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800542-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011785.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
```

```
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Barber JR,  Chang SM,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J;
XX
DR   WPI; 1998-086967/08.
XX
PT   New replication defective recombinant retroviruses - which express B
PT   domain-deleted human factor VIII or human factor IX for the treatment of
PT   haemophilia.
XX
PS   Example 31; Page 144; 236pp; English.
XX
CC   As apolipoprotein E (ApoE) enhancer cassette was generated from a set of
CC   4 synthetic oligonucleotides (see AAV15382-85) that span the entire
CC   sequence. The oligonucleotides were phosphorylated at the 5' end. The
CC   first oligonucleotide (AAV15382) is the sense strand and contains a 5'
CC   HindIII site. The ApoE enhancer cassette was used, together with a liver-
CC   specific alpha-1-antitrypsin promoter, to control expression of
CC   interferon sequences in retroviral vectors. The invention relates to new
CC   recombinant gene delivery vehicles, such as replication-defective
CC   retroviral vectors, and their use in gene therapy of genetic diseases
XX
SQ   Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 10
AAV15386
ID   AAV15386 standard; DNA; 90 BP.
XX
AC   AAV15386;
XX
DT   20-JUL-1998  (first entry)
XX
DE   ApoE enhancer sense oligonucleotide.
XX
KW   Interferon; human; gene therapy; retrovirus; vector; apolipoprotein E;
KW   ApoE; enhancer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800542-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011785.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Barber JR,  Chang SM,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J;
XX
DR   WPI; 1998-086967/08.
```

```
XX
PT   New replication defective recombinant retroviruses - which express B
PT   domain-deleted human factor VIII or human factor IX for the treatment of
PT   haemophilia.
XX
PS   Example 31; Page 146; 236pp; English.
XX
CC   As apolipoprotein E (ApoE) enhancer cassette was generated from a set of
CC   4 synthetic oligonucleotides (see AAV15386-89) that span the entire
CC   sequence. The oligonucleotides were phosphorylated at the 5' end. The
CC   first oligonucleotide (AAV15386) is the sense strand and contains a 5'
CC   EcoRI site. The ApoE enhancer cassette was used, together with a liver-
CC   specific alpha-1-antitrypsin promoter, to control expression of
CC   interferon sequences in retroviral vectors. The invention relates to new
CC   recombinant gene delivery vehicles, such as replication-defective
CC   retroviral vectors, and their use in gene therapy of genetic diseases
XX
SQ   Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 11
ADU47587
ID   ADU47587 standard; DNA; 90 BP.
XX
AC   ADU47587;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Oligonucleotide #5 used to generate ApoE enhancer cassette.
XX
KW   Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;
KW   thymidine kinase; TK; ss; apolipoprotein B; Apo E.
XX
OS   Unidentified.
XX
PN   US6818439-B1.
XX
PD   16-NOV-2004.
XX
PF   30-DEC-1997;   97US-00001039.
XX
PR   30-DEC-1994;   94US-00367071.
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Chang S,  Respess JG,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Greengard J,  Will L;
XX
DR   WPI; 2004-793566/78.
XX
PT   New high titre TK-1 retroviral vector expressing a factor VIII protein,
PT   useful in preparing a composition for treating hemophilia or thrombosis.
XX
PS   Example 33; SEQ ID NO 65; 138pp; English.
XX
CC   The present invention provides methods for obtaining measurable levels of
CC   a protein, nucleic acid molecule or enzymatic product in a bodily fluid
CC   or cells of a human. The method involves administering to a human a
```

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CC   recombinant retroviral preparation having a titer on HT1080 cells of
CC   greater than 10 5 cfu/ml where the recombinant retroviral preparation is
CC   capable of directing the expression of a protein, nucleic acid molecule
CC   or enzyme which generates an enzymatic product such that measurable
CC   levels of the protein, nucleic acid molecule or enzymatic product may be
CC   obtained in the bodily fluid or cells of the human. The invention also
CC   relates to a novel TK (thymidine kinase)-1 retroviral vector which
CC   expresses a factor VIII protein. The TK-1 retroviral vector is useful in
CC   preparing a composition for treating haemophilia, thrombosis and other
CC   disorders. The invention is useful in gene therapy. The present sequence
CC   is an oligonucleotide used to generate apolipoprotein E (Apo E) enhancer
CC   cassette. This sequence is used in the method for administration of
CC   recombinant gene delivery vehicles for the treatment of haemophilia and
CC   other disorders.
XX
SQ   Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 13;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 12
ADU47583
ID   ADU47583 standard; DNA; 90 BP.
XX
AC   ADU47583;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Oligonucleotide #1 used to generate ApoE enhancer cassette.
XX
KW   Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;
KW   thymidine kinase; TK; ss; apolipoprotein E; Apo E.
XX
OS   Unidentified.
XX
PN   US6818439-B1.
XX
PD   16-NOV-2004.
XX
PF   30-DEC-1997;   97US-00001039.
XX
PR   30-DEC-1994;   94US-00367071.
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Chang S,  Respess JG,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Greengard J,  Will L;
XX
DR   WPI; 2004-793566/78.
XX
PT   New high titre TK-1 retroviral vector expressing a factor VIII protein,
PT   useful in preparing a composition for treating hemophilia or thrombosis.
XX
PS   Example 33; SEQ ID NO 61; 138pp; English.
XX
CC   The present invention provides methods for obtaining measurable levels of
CC   a protein, nucleic acid molecule or enzymatic product in a bodily fluid
CC   or cells of a human. The method involves administering to a human a
CC   recombinant retroviral preparation having a titer on HT1080 cells of
CC   greater than 10 5 cfu/ml where the recombinant retroviral preparation is
```

```
CC   capable of directing the expression of a protein, nucleic acid molecule
CC   or enzyme which generates an enzymatic product such that measurable
CC   levels of the protein, nucleic acid molecule or enzymatic product may be
CC   obtained in the bodily fluid or cells of the human. The invention also
CC   relates to a novel TK (thymidine kinase)-1 retroviral vector which
CC   expresses a factor VIII protein. The TK-1 retroviral vector is useful in
CC   preparing a composition for treating haemophilia, thrombosis and other
CC   disorders. The invention is useful in gene therapy. The present sequence
CC   is an oligonucleotide used to generate apolipoprotein E (Apo E) enhancer
CC   cassette. This sequence is used in the method for administration of
CC   recombinant gene delivery vehicles for the treatment of haemophilia and
CC   other disorders.
XX
SQ   Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 82;  DB 13;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 13
AAV19599/c
ID   AAV19599 standard; DNA; 82 BP.
XX
AC   AAV19599;
XX
DT   25-MAR-2003  (revised)
DT   06-AUG-1998  (first entry)
XX
DE   Apolipoprotein E (Apo E) enhancer sequence generating antisense primer 3.
XX
KW   Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW   haemophilia; thrombosis; hypercoagulable disorder; liver disease;
KW   hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human;
KW   cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi;
KW   diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection;
KW   anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;
KW   autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E;
KW   enhancer sequence; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800541-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011784.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Barber JR,  Chang SMW,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J,  Lee R;
XX
DR   WPI; 1998-086966/08.
XX
PT   New replication defective recombinant retro-viruses - which can be
PT   administered to provide long term systemic expression of therapeutic
PT   protein in blood, useful in, e.g. treating hyper-coagulable disorders.
XX
```

```
PS   Example 33; Page 178; 272pp; English.
XX
CC   This primer is used for generating the apolipoprotein E (Apo E) enhancer
CC   sequence. This is used to construct a retroviral vector backbone with a
CC   liver specific promoter. The invention provides the preparation of
CC   replication defective recombinant retrovirus (RRV) expressing a
CC   therapeutic protein. The RRV preparation is resistant to degradation by
CC   human complement and is capable of inducing long term systemic expression
CC   of the therapeutic protein when administered intravenously to a human.
CC   The long term systemic expression results in a measurable level of the
CC   therapeutic protein being produced in the blood of the human for a period
CC   of at least 30 days after the administration of the RRV vector
CC   preparation. The RRV's can be used for in vivo delivery of therapeutic
CC   protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
CC   hypercoagulable disorders, liver diseases such as hepatitis, disorders
CC   such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
CC   combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular
CC   Dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
CC   hypopituitarism, adenine deaminase deficiency, alpha1-antitrypsin
CC   deficiency, Guacher's syndrome, anaemia, infections such as HIV
CC   infection, high blood pressure, Alzheimer's disease, autoimmune or
CC   inflammatory disease or graft versus host disease. RRV's are capable of
CC   surviving inactivation in human serum thereby allowing efficient gene
CC   transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 78;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-15;
  Matches   78;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         75 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 23

Qy        135 GGTCAGAGACCTCTCTGG 152
              ||||||||||||||||||
Db         22 GGTCAGAGACCTCTCTGG 5


RESULT 14
ADU47589/c
ID   ADU47589 standard; DNA; 82 BP.
XX
AC   ADU47589;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Oligonucleotide #7 used to generate ApoE enhancer cassette.
XX
KW   Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;
KW   thymidine kinase; TK; ss; apolipoprotein E; Apo E.
XX
OS   Unidentified.
XX
PN   US6818439-B1.
XX
PD   16-NOV-2004.
XX
PF   30-DEC-1997;   97US-00001039.
XX
PR   30-DEC-1994;   94US-00367071.
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ,  Chang S,  Respess JG,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Greengard J,  Will L;
XX
DR   WPI; 2004-793566/78.
```

```
XX
PT   New high titre TK-1 retroviral vector expressing a factor VIII protein,
PT   useful in preparing a composition for treating hemophilia or thrombosis.
XX
PS   Example 33; SEQ ID NO 67; 138pp; English.
XX
CC   The present invention provides methods for obtaining measurable levels of
CC   a protein, nucleic acid molecule or enzymatic product in a bodily fluid
CC   or cells of a human. The method involves administering to a human a
CC   recombinant retroviral preparation having a titer on HT1080 cells of
CC   greater than 10 5 cfu/ml where the recombinant retroviral preparation is
CC   capable of directing the expression of a protein, nucleic acid molecule
CC   or enzyme which generates an enzymatic product such that measurable
CC   levels of the protein, nucleic acid molecule or enzymatic product may be
CC   obtained in the bodily fluid or cells of the human. The invention also
CC   relates to a novel TK (thymidine kinase)-1 retroviral vector which
CC   expresses a factor VIII protein. The TK-1 retroviral vector is useful in
CC   preparing a composition for treating haemophilia, thrombosis and other
CC   disorders. The invention is useful in gene therapy. The present sequence
CC   is an oligonucleotide used to generate apolipoprotein E (Apo E) enhancer
CC   cassette. This sequence is used in the method for administration of
CC   recombinant gene delivery vehicles for the treatment of haemophilia and
CC   other disorders.
XX
SQ   Sequence 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 78;  DB 13;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-15;
  Matches   78;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         75 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 23

Qy        135 GGTCAGAGACCTCTCTGG 152
              ||||||||||||||||||
Db         22 GGTCAGAGACCTCTCTGG 5


RESULT 15
AAV19595/c
ID   AAV19595 standard; DNA; 82 BP.
XX
AC   AAV19595;
XX
DT   25-MAR-2003  (revised)
DT   06-AUG-1998  (first entry)
XX
DE   Apolipoprotein E (Apo E) enhancer sequence generating antisense primer 1.
XX
KW   Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW   haemophilia; thrombosis; hypercoagulable disorder; liver disease;
KW   hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human;
KW   cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi;
KW   diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection;
KW   anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;
KW   autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E;
KW   enhancer sequence; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9800541-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997;   97WO-US011784.
XX
PR   03-JUL-1996;   96US-00645601.
PR   13-AUG-1996;   96US-00696381.
PR   04-JUN-1997;   97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
```

```
XX
PI   Jolly DJ,  Barber JR,  Chang SMW,  Respess JG,  Allen JR,  Boder M;
PI   Chong K,  De La Vega D,  Depolo NJ,  Hsu DC,  Ibanez CE;
PI   Mittelstaedt DM,  Prussak CE,  Greengard J,  Lee R;
XX
DR   WPI; 1998-086966/08.
XX
PT   New replication defective recombinant retro-viruses - which can be
PT   administered to provide long term systemic expression of therapeutic
PT   protein in blood, useful in, e.g. treating hyper-coagulable disorders.
XX
PS   Example 33; Page 177; 272pp; English.
XX
CC   This primer is used for generating the apolipoprotein E (Apo E) enhancer
CC   sequence. This is used to construct a retroviral vector backbone with a
CC   liver specific promoter. The invention provides the preparation of
CC   replication defective recombinant retrovirus (RRV) expressing a
CC   therapeutic protein. The RRV preparation is resistant to degradation by
CC   human complement and is capable of inducing long term systemic expression
CC   of the therapeutic protein when administered intravenously to a human.
CC   The long term systemic expression results in a measurable level of the
CC   therapeutic protein being produced in the blood of the human for a period
CC   of at least 30 days after the administration of the RRV vector
CC   preparation. The RRV's can be used for in vivo delivery of therapeutic
CC   protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
CC   hypercoagulable disorders, liver diseases such as hepatitis, disorders
CC   such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
CC   combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular
CC   Dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
CC   hypopituitarism, adenine deaminase deficiency, alphal-antitrypsin
CC   deficiency, Guacher's syndrome, anaemia, infections such as HIV
CC   infection, high blood pressure, Alzheimer's disease, autoimmune or
CC   inflammatory disease or graft versus host disease. RRV's are capable of
CC   surviving inactivation in human serum thereby allowing efficient gene
CC   transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 82 BP; 12 A; 21 C; 27 G; 22 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 77;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-15;
  Matches   77;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         75 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 23

Qy        135 GGTCAGAGACCTCTCTG 151
              |||||||||||||||||
Db         22 GGTCAGAGACCTCTCTG 6


Search completed: April 18, 2006, 13:22:04
Job time : 95.4261 secs
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                         GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:          April 18, 2006, 12:18:29 ; Search time 747.823 Seconds
                                            (without alignments)
                                            9634.919 Million cell updates/sec

Title:           US-09-884-901A-8
Perfect score:   154
Sequence:        1 gtttgtgtgctgcctctgaa..........ggtcagagacctctctgggc 154

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:      82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                 1:  gb_est1:*
                 2:  gb_est2:*
                 3:  gb_est3:*
                 4:  gb_htc:*
                 5:  gb_est4:*
                 6:  gb_est5:*
                 7:  gb_est6:*
                 8:  gb_est7:*
                 9:  gb_gss1:*
                 10:  gb_gss2:*
                 11:  gb_gss3:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                      %
Result               Query
  No.     Score     Match Length DB  ID                         Description
  ----------------------------------------------------------------------------
c   1       38      24.7     958 10   CNS0044W                   AL066467 Drosophil
c   2     36.2      23.5     329 6   CB458659                   CB458659 717364 MA
c   3     35.6      23.1     643 1   AU279008                   AU279008 AU279008
    4     35.4      23.0     469 8   CX307208                   CX307208 C19002D06
c   5     35.2      22.9     363 7   CK779717                   CK779717 UMC-bend_
    6     35.2      22.9     401 7   CO727732                   CO727732 UMC-bend_
    7     35.2      22.9     479 2   BF042501                   BF042501 BP250012A
c   8     35.2      22.9     567 1   AU279081                   AU279081 AU279081
    9     35.2      22.9     579 2   BF043702                   BF043702 BP250015B
   10     35.2      22.9     615 6   CB434484                   CB434484 611104 MA
   11     35.2      22.9     716 6   CB457803                   CB457803 715917 MA
   12     35.2      22.9     732 7   CK970120                   CK970120 4085432 B
   13     35.2      22.9     742 7   CK834244                   CK834244 4058470 B
   14     35.2      22.9     825 8   DN526096                   DN526096 1270831 M
c  15     35.2      22.9     941 8   DN523404                   DN523404 1266895 M
c  16       35      22.7     554 9   AQ992245                   AQ992245 nbeb0085I
c  17       35      22.7     735 2   BE263325                   BE263325 601190812
c  18       35      22.7    1014 2   BG751214                   BG751214 602730325
c  19     34.2      22.2     792 11   CR806205                   CR806205 GR0AAA28A
c  20       34      22.1     289 9   AZ096407                   AZ096407 RPCI-23-4
   21     33.8      21.9     737 10   AG406290                   AG406290 Mus muscu
   22     33.8      21.9    1346 2   BG495013                   BG495013 602541679
c  23     33.6      21.8     311 6   CB696796                   CB696796 AMGNNUC:M
   24     33.6      21.8     335 1   AW631727                   AW631727 90990 MAR
c  25     33.6      21.8     432 8   R48041                     R48041 yj66d07.r1
   26     33.6      21.8     838 5   BU326878                   BU326878 603490651
   27     33.6      21.8     972 5   BU356799                   BU356799 603475259
c  28     33.4      21.7     430 2   BF501783                   BF501783 AT17336.5
c  29     33.4      21.7     528 2   BF498419                   BF498419 AT12812.5
c  30     33.4      21.7     549 2   BE978332                   BE978332 bs77b09.y
c  31     33.4      21.7     617 10   CL719165                   CL719165 OR_BBa004
c  32     33.4      21.7     639 10   CL746108                   CL746108 OR_BBa008
c  33     33.4      21.7     667 10   CL770284                   CL770284 OR_BBa014
c  34     33.4      21.7     764 10   CL712133                   CL712133 OR_BBa003
c  35     33.4      21.7     835 10   CL726784                   CL726784 OR_BBa005
c  36     33.4      21.7    2775 10   CL965232                   CL965232 OsIFCC011
c  37     32.8      21.3     444 5   BY388939                   BY388939 BY388939
c  38     32.8      21.3     477 9   AZ787078                   AZ787078 2M0032M19
c  39     32.8      21.3     554 3   BJ554747                   BJ554747 BJ554747
   40     32.8      21.3     583 10   AG973280                   AG973280 Drosophil
   41     32.8      21.3     623 10   AG970743                   AG970743 Drosophil
c  42     32.8      21.3    1049 3   BM423372                   BM423372 AGENCOURT
   43     32.4      21.0     467 3   BP614956                   BP614956 BP614956
c  44     32.4      21.0     640 9   CE010717                   CE010717 tigr-gss-
   45     32.4      21.0     752 7   CF951791                   CF951791 UI-M-HL0-

                                  ALIGNMENTS


RESULT 1
CNS0044W/c
LOCUS       CNS0044W                 958 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR09M23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL066467
VERSION     AL066467.1  GI:4942910
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 958)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..958
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR09M23"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN
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  Query Match             24.7%;  Score 38;  DB 10;  Length 958;
  Best Local Similarity   38.9%;  Pred. No. 2;
  Matches   49;  Conservative   29;  Mismatches   48;  Indels    0;  Gaps    0;

Qy           2 TTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAA 61
               ||| | |  | : | :   |  ||:::  |||:|| ||  :|: |  |||| ||: |||
Db         684 TTTTTTTTATWYTTTHCGTGGGCAMMMAAAACWAATTTTKCMCAAMCATGCCCMAAAAT 625

Qy          62 TGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTG 121
               ||: |||:: :: | |::   :||  .:::| | : : :::: :  |:|       |||
Db         624 TGSCCAAWSGWKCCCARYTWWMAAATHYMWAAAAWWMMMMKNVDNGSCCCAGCTTCTTT 565

Qy         122 GAGCTG 127
               |||:||
Db         564 GAGMTG 559


RESULT 2
CB458659/c
LOCUS       CB458659                 329 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  717364 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   CB458659
VERSION     CB458659.1  GI:29265043
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8072  row: D  column: 12
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             23.5%;  Score 36.2;  DB 6;  Length 329;
  Best Local Similarity   59.0%;  Pred. No. 5.5;
  Matches   62;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         112 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 53

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTG 115
               | |  |  ||| |   |  |||||   |     ||   |||||||
Db          52 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCTG 8


RESULT 3
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AU279008/c
LOCUS       AU279008                 643 bp    mRNA    linear   EST 02-JUL-2002
DEFINITION  AU279008 Cloned bovine placenta cDNA Bos taurus cDNA clone
            placenta1366 3', mRNA sequence.
ACCESSION   AU279008
VERSION     AU279008.1  GI:21682318
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and
            Sasaki,Y.
  TITLE     EST analysis of cloned bovine fetus and placenta
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Masahito Oishi
            Graduate School of Agriculture
            Kyoto University
            Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-6331
            Fax: 81-75-753-6340
            Email: oishi@jkans.jkans.kais.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="placenta1366"
                     /dev_stage="60 embryonic day"
                     /clone_lib="Cloned bovine placenta cDNA"
ORIGIN

  Query Match             23.1%;  Score 35.6;  DB 1;  Length 643;
  Best Local Similarity   58.5%;  Pred. No. 9.7;
  Matches   62;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         176 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 117

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
               | |  |  ||| |   |  |||||   |     ||   |||||| |
Db         116 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCTTA 71


RESULT 4
CX307208
LOCUS       CX307208                 469 bp    mRNA    linear   EST 06-MAY-2005
DEFINITION  C19002D06T7 FlavFrSub1 Citrus clementina x Citrus tangerina cDNA
            clone C19002D06, mRNA sequence.
ACCESSION   CX307208
VERSION     CX307208.1  GI:63076062
KEYWORDS    EST.
SOURCE      Citrus clementina x Citrus tangerina
  ORGANISM  Citrus clementina x Citrus tangerina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Forment,J., Gadea,J., Huerta,L., Abizanda,L., Agusti,J., Alamar,S.,
            Alos,E., Andres,F., Arribas,R., Beltran,J.P., Berbel,A.,
            Blazquez,M.A., Brumos,J., Canas,L.A., Cercos,M.,
            Colmenero-Flores,J.M., Conesa,A., Estables,B., Gandia,M.,
            Garcia-Martinez,J.L., Gimeno,J., Gisbert,A., Gomez,G.,
            Gonzalez-Candelas,L., Granell,A., Guerri,J., Lafuente,M.T.,
            Madueno,F., Marcos,J.F., Marques,M.C., Martinez,F.,
            Martinez-Godoy,M.A., Miralles,S., Moreno,P., Navarro,L., Pallas,V.,
            Perez-Amador,M.A., Perez-Valle,J., Pons,C., Rodrigo,I.,
            Rodriguez,P.L., Royo,C., Serrano,R., Soler,G., Tadeo,F., Talon,M.,
            Terol,J., Trenor,M., Vaello,L., Vicente,O., Vidal,Ch., Zacarias,L.
            and Conejero,V.
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  TITLE     Development of a citrus genome-wide EST collection and cDNA
            microarray as resources for genomic studies
  JOURNAL   Plant Mol. Biol. 57 (3), 375-391 (2005)
   PUBMED   15830128
COMMENT     Contact: Forment J
            Genomics Laboratory
            Instituto de Biologia Molecular y Celular de Plantas (Universidad
            Politecnica de Valencia - Consejo Superior de Investigaciones
            Cientificas)
            Avenida de los Naranjos s/n, 46022 Valencia, Spain
            Email: jforment@ibmcp.upv.es.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Citrus clementina x Citrus tangerina"
                     /mol_type="mRNA"
                     /cultivar="Fortune"
                     /db_xref="taxon:307631"
                     /clone="C19002D06"
                     /sex="hermaphrodite"
                     /tissue_type="flavedo"
                     /dev_stage="adult trees"
                     /lab_host="Escherichia coli"
                     /clone_lib="FlavFrSub1"
                     /note="Organ: fruits; Vector: pCR2.1; Subtracted cDNA
                     library made from poly-A+ RNA from flavedo of fruits
                     stored at 2oC for 14 days, subtracted with poly-A+ RNA
                     from fruits stored at 12oC for 14 days"
ORIGIN

  Query Match             23.0%;  Score 35.4;  DB 8;  Length 469;
  Best Local Similarity   55.2%;  Pred. No. 10;
  Matches   69;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps , 0;

Qy         29 TGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACATTGCAAGCAGCAAACAG 88
              || |   | ||  || || |||  |  | || |   | | |    || ||||| ||||| 
Db        248 TGTATTCATTTGCGCGTAATCAACTGTCCAAGAATAGAAGAAGCAGCGAGCAGAAAACAA 307

Qy         89 CAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAGACCTCT 148
                ||    ||||   | |||||| | | ||  |  ||  || ||   ||| || ||||  
Db        308 TGAAGCAGCAGCTAACACTGCCTACAGGCCCGGCTGCGTGGCCAATAGTCGGAAACCTTC 367

Qy        149 CTGGG 153
              | | |
Db        368 CAGAG 372


RESULT 5
CK779717/c
LOCUS       CK779717                 363 bp    mRNA    linear   EST 23-FEB-2004
DEFINITION  UMC-bend_0B01-012-g01 Day 8 Uterus bend Bos taurus cDNA 3', mRNA
            sequence.
ACCESSION   CK779717
VERSION     CK779717.1  GI:42745395
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
            Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  TITLE     USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
            Reproduction
  JOURNAL   Unpublished (2002)
COMMENT     Contact: DNA Core Facility (Bovine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: bovine@rnet.missouri.edu
            POLYA=Yes.
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FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone_lib="bend"
                     /note="Funding: The production of ESTs submitted in this
                     project was funded by USDA Grant MRI-2002-03476 entitled
                     'Bovine ESTs: Focus on Female Reproduction' to RS Prather,
                     E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts,
                     MF Smith and RS Youngquist. Genetic Source: Heifers for
                     the project were purchased from Circle A Ranch, Iberia, MO
                     (http://www.circlearanch.com/home.html). These heifers,
                     while not registered have known Angus pedigrees going back
                     at least 4 generations. Samples collected: The samples
                     consisted of the following: germinal vesicle-stage
                     oocytes; in vitro derived embryos (2-cell, morula,
                     blastocyst and nuclear transfer blastocyst); in vivo
                     blastocysts and conceptuses (days 8, 14, 16 and 18);
                     corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                     follicles (days 0, non-recruited, recruited, early
                     selected and preovulatory); oviduct (days 0, 3 and 5);
                     endometrium (days 5, 8, 14, 16, 18 and 35); and
                     placenta/embryo from day 35 conceptuses. Expanded
                     descriptions of how the tissues were collected can be
                     found at the following URL:
                     http://genome.rnet.missouri.edu/Bovine/Methods.html.
                     Library construction (Standard Protocol): All procedures
                     have been described in detail elsewhere (Soares et al.,
                     1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                     cellular RNA from each sample was isolated by using
                     STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                     poly(A)+ RNA was obtained by two rounds of purification
                     with the Oligotex mRNA isolation kit (Qiagen) according to
                     the manufacturer''s instructions. The libraries were
                     constructed by E. Ferguson and R. Woods essentially as
                     described by the manufacturer's instructions provided with
                     the SuperScript Plasmid System (Invitrogen, cat. no.
                     18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at
                     c37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide.
                     (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at c37
                     degrees with SuperScript II (Invitrogen) reverse
                     transcriptase (Jiang et al., 2001). The 'tag' represents a
                     tissue/stage-specific ten-base sequence identifier
                     (http://genome.uiowa.edu/pubsoft/software.html) present in
                     the oligonucleotide used to prime first-strand synthesis.
                     Second strand synthesis was performed with T4 DNA
                     polymerase in the presence of DNA ligase and RNase H.
                     After second strand synthesis, the double-stranded cDNAs
                     were ligated to SalI adapters (Invitrogen-Life
                     Technologies) and digested with NotI. The cDNAs were size
                     selected by passage through cDNA size fractionation
                     columns (Invitrogen-Life technologies). The cDNAs derived
                     from each developmental stage of a particular tissue were
                     mixed on an equimolar basis and ligated directionally into
                     the NotI and SalI sites of the pCMV-SPORT6 vector
                     (Invitrogen). After ligation of the inserts, the plasmids
                     were electroporated into DH10B bacteria. Library
                     Construction (PCR Protocol): The amount of mRNA that was
                     recovered from oocytes and embryos was quite limiting and
                     was not sufficient for library production with the
                     standard protocol. Therefore, PCR-based protocol was
                     utilized for producing libraries from sources in which the
                     amount of extracted mRNA was small (oocytes and embryos).
                     Poly-A RNA was isolated by using the MicroPoly(A) Pure kit
                     from Ambion (cat. # 1918). The mRNA was reverse
                     transcribed with a NotI-tag-dT18 oligonucleotide and a
                     SMART oligonucleotide (Clontech) modified to contain a
                     SalI site to generate full-length cDNA with a sequence
                     complementary to the SMART oligonucleotide. Sequences
                     within the SMART and dT oligonucleotides were used as
                     primers to amplify the cDNAs by PCR with pfu turbo
                     polymerase (Stratagene). The resulting PCR products were
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                      purified, digested with NotI and SalI and size
                      fractionated by using Chroma Spin-1000 columns (Clontech).
                      Purified cDNA from each PCR reaction was quantitated and
                      mixed on an equimolar basis for ligation into the pCMV-
                      SPORT6 vector. Preliminary Library Characterization:
                      Randomly chosen clones from each library were analyzed by
                      restriction digestion to determine average insert size (96
                      clones) and by sequencing (~4 96-well plates) to confirm
                      library quality [e.g. the presence of short polyA+ tails,
                      genomic DNA contamination (must be <1%), ribosomal RNA
                      clones (must be <1%), etc.] and to provide a sequence
                      database representing the predominant clones in each
                      library. The clones were sequenced at the University of
                      Missouri-Columbia DNA Core Facility. After production of
                      the libraries, equal numbers of recombinants from each
                      library were pooled to produce a single mixed library
                      (mega-library) for more extensive sequencing.
                      Bioinformatics work was performed by GK Springer's
                      bioinformatics group (Spollen WG, Topinka CM, Khambati AA)
                      in Computer Science at the University of
                      Missouri-Columbia. Clone Requests: Requests for clones
                      should be made to the Director of the University of
                      Missouri DNA Core facility at: bovine@rnet.missouri.edu.
                      Bonaldo MF, Lennon G, Soares MB,. Normalization and
                      Subtraction: Two approaches to facilitate gene discovery.
                      Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE,
                      Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion
                      BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing
                      cDNA libraries with fewer clones that contain long
                      poly(dA) tails.  Biotechniques 31:38-42. Soares MB, MF
                      Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
                      Construction and characterization of a normalized cDNA
                      library.  Proc Natl Acad Sci, 91:9228-9232.
                      TAG_TISSUE=Day 8 Uterus
                      TAG_SEQ=CTGACACTTG"
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 7;  Length 363;
  Best Local Similarity   58.7%;  Pred. No. 11;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db        104 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 45

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
              | |  |  ||| |   |  |||||   |     ||   ||||||
Db         44 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 1


RESULT 6
CO727732
LOCUS       CO727732                 401 bp    mRNA    linear   EST 27-JUL-2004
DEFINITION  UMC-bend_0A02-023-b04 Uterus (endometium) bend Bos taurus cDNA 3',
            mRNA sequence.
ACCESSION   CO727732
VERSION     CO727732.1  GI:50710669
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
            Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  TITLE     USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
            Reproduction
  JOURNAL   Unpublished (2002)
COMMENT     Contact: DNA Core Facility (Bovine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
```

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            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: bovine@rnet.missouri.edu
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..401
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone_lib="bend"
                     /note="Funding: The production of ESTs submitted in this
                     project was funded by USDA Grant MRI-2002-03476 entitled
                     'Bovine ESTs: Focus on Female Reproduction' to RS Prather,
                     E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts,
                     MF Smith and RS Youngquist. Genetic Source: Heifers for
                     the project were purchased from Circle A Ranch, Iberia, MO
                     (http://www.circlearanch.com/home.html). These heifers,
                     while not registered have known Angus pedigrees going back
                     at least 4 generations. Samples collected: The samples
                     consisted of the following: germinal vesicle-stage
                     oocytes; in vitro derived embryos (2-cell, morula,
                     blastocyst and nuclear transfer blastocyst); in vivo
                     blastocysts and conceptuses (days 8, 14, 16 and 18);
                     corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                     follicles (days 0, non-recruited, recruited, early
                     selected and preovulatory); oviduct (days 0, 3 and 5);
                     endometrium (days 5, 8, 14, 16, 18 and 35); and
                     placenta/embryo from day 35 conceptuses. Expanded
                     descriptions of how the tissues were collected can be
                     found at the following URL:
                     http://genome.rnet.missouri.edu/Bovine/Methods.html.
                     Library construction (Standard Protocol): All procedures
                     have been described in detail elsewhere (Soares et al.,
                     1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                     cellular RNA from each sample was isolated by using
                     STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                     poly(A)+ RNA was obtained by two rounds of purification
                     with the Oligotex mRNA isolation kit (Qiagen) according to
                     the manufacturer''s instructions. The libraries were
                     constructed by E. Ferguson and R. Woods essentially as
                     described by the manufacturer's instructions provided with
                     the SuperScript Plasmid System (Invitrogen, cat. no.
                     18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at
                     c37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide
                     (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at c37
                     degrees with SuperScript II (Invitrogen) reverse
                     transcriptase (Jiang et al., 2001). The 'tag' represents a
                     tissue/stage-specific ten-base sequence identifier
                     (http://genome.uiowa.edu/pubsoft/software.html) present in
                     the oligonucleotide used to prime first-strand synthesis.
                     Second strand synthesis was performed with T4 DNA
                     polymerase in the presence of DNA ligase and RNase H.
                     After second strand synthesis, the double-stranded cDNAs
                     were ligated to SalI adapters (Invitrogen-Life
                     Technologies) and digested with NotI. The cDNAs were size
                     selected by passage through cDNA size fractionation
                     columns (Invitrogen-Life technologies). The cDNAs derived
                     from each developmental stage of a particular tissue were
                     mixed on an equimolar basis and ligated directionally into
                     the NotI and SalI sites of the pCMV-SPORT6 vector
                     (Invitrogen). After ligation of the inserts, the plasmids
                     were electroporated into DH10B bacteria. Library
                     Construction (PCR Protocol): The amount of mRNA that was
                     recovered from oocytes and embryos was quite limiting and
                     was not sufficient for library production with the
                     standard protocol. Therefore, PCR-based protocol was
                     utilized for producing libraries from sources in which the
                     amount of extracted mRNA was small (oocytes and embryos).
                     Poly-A RNA was isolated by using the MicroPoly(A) Pure kit
                     from Ambion (cat. # 1918). The mRNA was reverse
                     transcribed with a NotI-tag-dT18 oligonucleotide and a
                     SMART oligonucleotide (Clontech) modified to contain a
                     SalI site to generate full-length cDNA with a sequence
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                    complementary to the SMART oligonucleotide. Sequences
                    within the SMART and dT oligonucleotides were used as
                    primers to amplify the cDNAs by PCR with pfu turbo
                    polymerase (Stratagene). The resulting PCR products were
                    purified, digested with NotI and SalI and size
                    fractionated by using Chroma Spin-1000 columns (Clontech).
                    Purified cDNA from each PCR reaction was quantitated and
                    mixed on an equimolar basis for ligation into the pCMV-
                    SPORT6 vector. Preliminary Library Characterization:
                    Randomly chosen clones from each library were analyzed by
                    restriction digestion to determine average insert size (96
                    clones) and by sequencing (~4 96-well plates) to confirm
                    library quality [e.g. the presence of short polyA+ tails,
                    genomic DNA contamination (must be <1%), ribosomal RNA
                    clones (must be <1%), etc.] and to provide a sequence
                    database representing the predominant clones in each
                    library. The clones were sequenced at the University of
                    Missouri-Columbia DNA Core Facility. After production of
                    the libraries, equal numbers of recombinants from each
                    library were pooled to produce a single mixed library
                    (mega-library) for more extensive sequencing.
                    Bioinformatics work was performed by GK Springer's
                    bioinformatics group (Spollen WG, Topinka CM, Khambati AA)
                    in Computer Science at the University of
                    Missouri-Columbia. Clone Requests: Requests for clones
                    should be made to the Director of the University of
                    Missouri DNA Core facility at: bovine@rnet.missouri.edu.
                    Bonaldo MF, Lennon G, Soares MB,. Normalization and
                    Subtraction: Two approaches to facilitate gene discovery.
                    Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE,
                    Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion
                    BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing
                    cDNA libraries with fewer clones that contain long
                    poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF
                    Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
                    Construction and characterization of a normalized cDNA
                    library. Proc Natl Acad Sci, 91:9228-9232.
                    TAG_SEQ=Not found"
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 7;  Length 401;
  Best Local Similarity   58.7%;  Pred. No. 12;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db        112 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 171

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
              | |  |  ||| |   |  |||||   |     ||   ||||||
Db        172 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 215


RESULT 7
BF042501
LOCUS       BF042501                 479 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  BP250012A10B5 Soares normalized bovine placenta Bos taurus cDNA
            clone BP250012A10B5 5', mRNA sequence.
ACCESSION   BF042501
VERSION     BF042501.1  GI:10759556
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
            Larson,J.H.
  TITLE     Bovine ESTs
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
```

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            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            This sequence is vector free and at least 200 bp in length.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 479   Std Error: 0.00
            Plate: BP250012A10  row: B  column: 5
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 479.
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="BP250012A10B5"
                     /sex="female"
                     /lab_host="DH10B"
                     /clone_lib="Soares normalized bovine placenta"
                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI; The cDNA library was contributed by the
                     Soares laboratory and it  was constructed and normalized
                     as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. "
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 2;  Length 479;
  Best Local Similarity   58.7%;  Pred. No. 12;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db        127 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 186

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
              | |  |  ||| |   |  |||||   |     ||   ||||||
Db        187 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 230


RESULT 8
AU279081/c
LOCUS       AU279081                 567 bp    mRNA    linear   EST 02-JUL-2002
DEFINITION  AU279081 Cloned bovine placenta cDNA Bos taurus cDNA clone
            placenta1520 3', mRNA sequence.
ACCESSION   AU279081
VERSION     AU279081.1  GI:21682391
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 567)
  AUTHORS   Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and
            Sasaki,Y.
  TITLE     EST analysis of cloned bovine fetus and placenta
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Masahito Oishi
            Graduate School of Agriculture
            Kyoto University
            Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-6331
            Fax: 81-75-753-6340
            Email: oishi@jkans.jkans.kais.kyoto-u.ac.jp.
```

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FEATURES             Location/Qualifiers
     source          1..567
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="placenta1520"
                     /dev_stage="60 embryonic day"
                     /clone_lib="Cloned bovine placenta cDNA"
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 1;  Length 567;
  Best Local Similarity   58.7%;  Pred. No. 12;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         105 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 46

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
               | |  |  ||| |   |  |||||   |     ||   ||||||
Db          45 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 2


RESULT 9
BF043702
LOCUS       BF043702                 579 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  BP250015B10E12 Soares normalized bovine placenta Bos taurus cDNA
            clone BP250015B10E12 5', mRNA sequence.
ACCESSION   BF043702
VERSION     BF043702.1  GI:10760757
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
            Larson,J.H.
  TITLE     Bovine ESTs
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            This sequence is vector free and at least 200 bp in length.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 579   Std Error: 0.00
            Plate: BP250015B10  row: E  column: 12
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 579.
FEATURES             Location/Qualifiers
     source          1..579
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="BP250015B10E12"
                     /sex="female"
                     /lab_host="DH10B"
                     /clone_lib="Soares normalized bovine placenta"
                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI; The cDNA library was contributed by the
```

```
                     Soares laboratory and it  was constructed and normalized
                     as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. "
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 2;  Length 579;
  Best Local Similarity   58.7%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         136 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 195

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
               | |  |  ||| |   |  |||||   |     ||   ||||||
Db         196 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 239


RESULT 10
CB434484
LOCUS       CB434484                 615 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  611104 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB434484
VERSION     CB434484.1  GI:29214562
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8034  row: P  column: 15
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1..615
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 6;  Length 615;
  Best Local Similarity   58.7%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         335 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 394

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
               | |  |  ||| |   |  |||||   |     ||   ||||||
Db         395 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 438
```

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RESULT 11
CB457803
LOCUS       CB457803                 716 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  715917 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB457803
VERSION     CB457803.1  GI:29264185
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 716)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8073  row: C  column: 5
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .716
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 6;  Length 716;
  Best Local Similarity   58.7%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         77 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 136

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
              | |  |  ||| |   |  |||||   |     ||   ||||||
Db        137 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 180


RESULT 12
CK970120
LOCUS       CK970120                 732 bp    mRNA    linear   EST 16-MAR-2004
DEFINITION  4085432 BARC 9BOV Bos taurus cDNA clone 9BOV2_A09 5', mRNA
            sequence.
ACCESSION   CK970120
VERSION     CK970120.1  GI:45488094
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
  TITLE     Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt " -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 2  row: A  column: 09
            Seq primer: CCCAGTCACGACGTTGTAAAACG
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="9BOV2_A09"
                     /sex="Male"
                     /tissue_type="Pooled"
                     /dev_stage="Multiple"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="BARC 9BOV"
                     /note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
                     Site_2: NotI; Equimolar amounts of mRNA extracted from
                     fundic and pyloric abomasums of 18 and 21 week old steers.
                     Exposure to Ostertagia ostertagi was initiated at 15 weeks
                     of age. fundic and pyloric abomasum"
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 7;  Length 732;
  Best Local Similarity   58.7%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              ||||   ||| |  | | | ||  ||||||||||| | ||| |||   ||||    ||||
Db         87 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 146

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
              | |  |  ||| |   |  |||||   |     ||   ||||||
Db        147 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 190


RESULT 13
CK834244
LOCUS       CK834244                 742 bp    mRNA    linear   EST 04-MAR-2004
DEFINITION  4058470 BARC 8BOV Bos taurus cDNA clone 8BOV_2D12 5', mRNA
            sequence.
ACCESSION   CK834244
VERSION     CK834244.1  GI:45064530
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
  TITLE     Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
```

```
            0.000925 using options -trim_alt '' -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 2  row: D  column: 12
            Seq primer: CCTATTTAGGTGACACTATAGAAC
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="8BOV_2D12"
                     /sex="Female"
                     /tissue_type="Epithelial, Muscle"
                     /dev_stage="Lactating, Neonatal"
                     /lab_host="DH10B TonA"
                     /clone_lib="BARC 8BOV"
                     /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
                     NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
                     library in pCMVsport6.1, constructed from equimolar mRNA
                     pools derived from 5 sources, 4 lactating intestinal, 1
                     neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                     Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                     Duodenum, Jejunum, Distal Ileum"
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 7;  Length 742;
  Best Local Similarity   58.7%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
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Db         599 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 658

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
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Db         659 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 702


RESULT 14
DN526096
LOCUS       DN526096                 825 bp    mRNA    linear   EST 11-MAR-2005
DEFINITION  1270831 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   DN526096
VERSION     DN526096.1  GI:60971328
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 825)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: RLK8044  row: A  column: 11
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
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                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
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ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 8;  Length 825;
  Best Local Similarity   58.7%;  Pred. No. 14;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

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Db         205 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 264

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
               | |  |  ||| |   |  |||||   |     ||   ||||||
Db         265 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 308


RESULT 15
DN523404/c
LOCUS       DN523404                 941 bp    mRNA    linear   EST 11-MAR-2005
DEFINITION  1266895 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   DN523404
VERSION     DN523404.1  GI:60966258
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: RLK8044  row: A  column: 11
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
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                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."
ORIGIN

  Query Match             22.9%;  Score 35.2;  DB 8;  Length 941;
  Best Local Similarity   58.7%;  Pred. No. 14;
  Matches   61;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

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Db         803 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 744

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
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Db        743 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 700

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Job time : 751.823 secs
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                    GenCore version 5.1.7
           Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:46:08 ; Search time 153.338 Seconds
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Perfect score:  154
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:      19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA_Main:*
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     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

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     3     154   100.0    771  3  US-09-884-901-4            Sequence 4, Appli
     4     154   100.0  10527  3  US-09-863-733A-100         Sequence 100, App
     5     154   100.0  10527  5  US-10-116-420-100          Sequence 100, App
     6     154   100.0  10527  6  US-10-287-964-95           Sequence 95, Appl
     7     154   100.0  16963  7  US-10-741-601-5756         Sequence 5756, Ap
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    14    32.2    20.9    645  4  US-09-925-065A-103589      Sequence 103589,
c   15    31.8    20.6    662  4  US-09-925-065A-782496      Sequence 782496,
c   16    31.6    20.5  31134  8  US-10-741-600-18001        Sequence 18001, A
c   17    31.4    20.4  88191  3  US-09-799-799-3            Sequence 3, Appli
    18    31.2    20.3    257  3  US-09-864-761-25083        Sequence 25083, A
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c   24      31    20.1   2018  7  US-10-302-172-433          Sequence 433, App
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c   26    30.8    20.0 170245  7  US-10-717-597-322          Sequence 322, App
    27    30.6    19.9    207  8  US-10-674-124A-17250       Sequence 17250, A
c   28    30.6    19.9  26993  6  US-10-004-113-13           Sequence 13, Appl
c   29    30.6    19.9  26993  7  US-10-394-948-7            Sequence 7, Appli
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    31    30.4    19.7    613  4  US-09-925-065A-757427      Sequence 757427,
c   32    30.4    19.7   1400  7  US-10-322-281-643          Sequence 643, App
c   33    30.4    19.7   2292  7  US-10-437-963-43156        Sequence 43156, A
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c   35    30.2    19.6    552  6  US-10-029-386-8280         Sequence 8280, Ap
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c   38      30    19.5    475  5  US-10-027-632-43555        Sequence 43555, A
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                               ALIGNMENTS


RESULT 1
US-09-884-901-8
; Sequence 8, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
;  APPLICANT: Miao, Carol
;  APPLICANT:  Kay, Mark
;  TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
;  FILE REFERENCE: UOFW-1-17396
;  CURRENT APPLICATION NUMBER: US/09/884,901
;  CURRENT FILING DATE:  2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/212,902
;  PRIOR FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 154
;   TYPE: DNA
;   ORGANISM: HomoSapien
US-09-884-901-8

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  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120

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RESULT 2
US-09-884-901-9
; Sequence 9, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
;  APPLICANT: Miao, Carol
;  APPLICANT:  Kay, Mark
;  TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
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;  FILE REFERENCE: UOFW-1-17396
;  CURRENT APPLICATION NUMBER: US/09/884,901
;  CURRENT FILING DATE:  2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/212,902
;  PRIOR FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 328
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-884-901-9

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  Best Local Similarity   100.0%;  Pred. No. 2.5e-43;
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Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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RESULT 3
US-09-884-901-4
; Sequence 4, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
;  APPLICANT: Miao, Carol
;  APPLICANT:  Kay, Mark
;  TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
;  FILE REFERENCE: UOFW-1-17396
;  CURRENT APPLICATION NUMBER: US/09/884,901
;  CURRENT FILING DATE:  2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/212,902
;  PRIOR FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 771
;   TYPE: DNA
;   ORGANISM: HomoSapien
US-09-884-901-4

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Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db        198 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 231


RESULT 4
US-09-863-733A-100
; Sequence 100, Application US/09863733A
; Publication No. US20030082537A1
; GENERAL INFORMATION:
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;  APPLICANT: Stanton, Jr., Vincent P.
;  TITLE OF INVENTION: METHODS FOR GENETIC ANALYSIS OF DNA
;  FILE REFERENCE: 11926-113001
;  CURRENT APPLICATION NUMBER: US/09/863,733A
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 09/697,028
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: 09/696,998
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: 09/697,013
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: 60/206,613
;  PRIOR FILING DATE: 2000-05-23
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
;   LENGTH: 10527
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-863-733A-100

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  Best Local Similarity   100.0%;  Pred. No. 7e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db       9728 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 9787

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db       9788 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 9821


RESULT 5
US-10-116-420-100
; Sequence 100, Application US/10116420
; Publication No. US20030073101A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Jr., Vincent P.
;  APPLICANT:  Olson, Jeffrey
;  APPLICANT:  Zillmann, Martin
;  TITLE OF INVENTION: RESTRICTION ENZYME GENOTYPING
;  FILE REFERENCE: 11926-167001
;  CURRENT APPLICATION NUMBER: US/10/116,420
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 09/863,733
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 09/697,028
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: US 09/696,998
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: US 09/697,013
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: US 60/206,613
;  PRIOR FILING DATE: 2000-05-23
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
;   LENGTH: 10527
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-116-420-100

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         9728 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 9787

Qy          121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
                ||||||||||||||||||||||||||||||||||
Db         9788 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 9821

RESULT 6
US-10-287-964-95
; Sequence 95, Application US/10287964
; Publication No. US20030219769A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Jeffrey
;  APPLICANT:  Zillmann, Martin
;  APPLICANT:  Stanton, Jr., Vincent P.
;  TITLE OF INVENTION: METHODS FOR GENETIC ANALYSIS OF DNA USING BIASED AMPLIFICATION OF
;  TITLE OF INVENTION:  POLYMORPHIC SITES
;  FILE REFERENCE: 11926-016002
;  CURRENT APPLICATION NUMBER: US/10/287,964
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 09/696,998
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: US 60/206,613
;  PRIOR FILING DATE: 2000-05-23
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 10527
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-287-964-95

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  Best Local Similarity   100.0%;  Pred. No. 7e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         9668 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 9727

Qy           61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         9728 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 9787

Qy          121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
                ||||||||||||||||||||||||||||||||||
Db         9788 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 9821

RESULT 7
US-10-741-601-5756
; Sequence 5756, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5756
;   LENGTH: 16963
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5756
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  Query Match             100.0%;  Score 154;  DB 7;  Length 16963;
  Best Local Similarity   100.0%;  Pred. No. 8e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        15958 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 16017

Qy           61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        16018 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 16077

Qy          121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
                ||||||||||||||||||||||||||||||||||
Db        16078 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 16111

RESULT 8
US-10-741-600-17945
; Sequence 17945, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17945
;   LENGTH: 16963
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-17945

  Query Match             100.0%;  Score 154;  DB 8;  Length 16963;
  Best Local Similarity   100.0%;  Pred. No. 8e-43;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        15958 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 16017

Qy           61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        16018 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 16077

Qy          121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
                ||||||||||||||||||||||||||||||||||
Db        16078 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 16111

RESULT 9
US-09-967-013-5
; Sequence 5, Application US/09967013
; Patent No. US20020045840A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Jr, Vincent P.
;  TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 11926-022001
;  CURRENT APPLICATION NUMBER: US/09/967,013
;  CURRENT FILING DATE:  2000-10-25
;  PRIOR APPLICATION NUMBER: 60/206,613
;  PRIOR FILING DATE: 2000-05-23
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 41907
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-967-013-5
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  Query Match             100.0%;  Score 154;  DB 3;  Length 41907;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-42;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36908 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 36967

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36968 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 37027

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      37028 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 37061


RESULT 10
US-10-100-235-11
; Sequence 11, Application US/10100235
; Publication No. US20030147853A1
; GENERAL INFORMATION:
;  APPLICANT: MCCLELLAND, Alan
;  APPLICANT:  SCOLLAY, Roland
;  TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS-MEDIATED GENE
;  TITLE OF INVENTION:  TRANSFER VIA RETRODUCTAL INFUSION OF VIRIONS
;  FILE REFERENCE: 0800-0027
;  CURRENT APPLICATION NUMBER: US/10/100,235
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: 60/275,908
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  ApoE HCR
US-10-100-235-11

  Query Match             98.1%;  Score 151;  DB 6;  Length 154;
  Best Local Similarity.  100.0%;  Pred. No. 2.2e-42;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 63

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 123

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
              |||||||||||||||||||||||||||||||
Db        124 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 154


RESULT 11
US-10-972-079-50807/c
; Sequence 50807, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  KERR, Richard
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  HOLM, Tom
;  TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
;  TITLE OF INVENTION:  LIVESTOCK
;  FILE REFERENCE: MMI1110-2
;  CURRENT APPLICATION NUMBER: US/10/972,079
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,333
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 96631
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 50807
;   LENGTH: 568
;   TYPE: DNA
;   ORGANISM: Chicken  19866894298036_5
US-10-972-079-50807

  Query Match             23.6%;  Score 36.4;  DB 9;  Length 568;
  Best Local Similarity   56.8%;  Pred. No. 0.037;
  Matches   67;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          7 GTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGC 66
              ||||||||  |  || |  | | |  | | | || ||     | |  ||    ||||| |
Db        465 GTGCTGCCATTACAGCCGGCGCGGCGCGAGCATCCGCGGCAGCGTCGCCTAGCAATGGCC 406

Qy         67 AAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAG 124
                ||  ||| ||||||  |   |  |  ||    || |||| ||| ||| || |||||
Db        405 GCACTCTGCCAGCAGCGCATCTCGCATGCAGGCACCACCCTCCCTCCTGCCCCTGGAG 348


RESULT 12
US-10-972-079-50806/c
; Sequence 50806, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  KERR, Richard
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  HOLM, Tom
;  TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEE
;  TITLE OF INVENTION:  LIVESTOCK
;  FILE REFERENCE: MMI1110-2
;  CURRENT APPLICATION NUMBER: US/10/972,079
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,333
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 96631
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 50806
;   LENGTH: 574
;   TYPE: DNA
;   ORGANISM: Chicken  19866894298036_4
US-10-972-079-50806

  Query Match             23.6%;  Score 36.4;  DB 9;  Length 574;
  Best Local Similarity   56.8%;  Pred. No. 0.037;
  Matches   67;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          7 GTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGC 66
              ||||||||  |  || |  | | |  | | | || ||     | |  ||    ||||| |
Db        471 GTGCTGCCATTACAGCCGGCGCGGCGCGAGCATCCGCGGCAGCGTCGCCTAGCAATGGCC 412

Qy         67 AAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAG 124
                ||  ||| ||||||  |   |  |  ||    || |||| ||| ||| || |||||
Db        411 GCACTCTGCCAGCAGCGCATCTCGCATGCAGGCACCACCCTCCCTCCTGCCCCTGGAG 354


RESULT 13
US-09-925-065A-103590
; Sequence 103590, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
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;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103590
;   LENGTH: 645
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-103590

  Query Match             21.2%;  Score 32.6;  DB 4;  Length 645;
  Best Local Similarity   58.9%;  Pred. No. 0.81;
  Matches   56;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
               | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | ||||| ||
Db          65 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCCTGCAGA 124

Qy         117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
                | | |    ||   |||||||| |      ||||
Db         125 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 159

RESULT 14
US-09-925-065A-103589
; Sequence 103589, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103589
;   LENGTH: 645
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-103589

  Query Match             20.9%;  Score 32.2;  DB 4;  Length 645;
  Best Local Similarity   57.9%;  Pred. No. 1.1;
  Matches   55;  Conservative    1;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
               | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | |:||| ||
Db          65 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCYTGCAGA 124

Qy         117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
                | | |    ||   |||||||| |      ||||
Db         125 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 159
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RESULT 15
US-09-925-065A-782496/c
; Sequence 782496, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 782496
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-782496

  Query Match             20.6%;  Score 31.8;  DB 4;  Length 662;
  Best Local Similarity   51.8%;  Pred. No. 1.6;
  Matches   72;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
               |||| ||| | |||| |||| |  |       |        | ||   ||||     |||
Db         141 TGCCACTGCACTCCAGACTGGATGACAGAGCGAGACTCAGTCTCTAAAAAAGAAAGAAAG 82

Qy          71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGG 130
               |    ||  || ||| |||| || || | |  | ||| ||    || || |||  |||
Db          81 AAAAGAAAAAGAAAATAGCAGACTCATATCTGTGCCTTCCCCTGGATCTGGGACGTGGCC 22

Qy         131 CAGAGGTCAGAGACCTCTC 149
                    |   ||| |||| |
Db          21 AGAGAGAGGGAGCCCTCCC 3

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters:     18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA_New:*
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               2:  /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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               4:  /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
               5:  /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
               6:  /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
               7:  /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
               8:  /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
               9:  /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
               10:  /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
               11:  /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
               12:  /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                    %
Result              Query
  No.     Score     Match Length DB  ID                      Description
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     1      154     100.0 153142 14  US-11-121-086-27         Sequence 27, Appl
     2    153.6     100.0  16963  8  US-10-995-561-13467     Sequence 13467, A
     3    153.6     100.0  40000  8  US-10-995-561-13513     Sequence 13513, A
     4    146.6      95.2    201  8  US-10-995-561-75740     Sequence 75740, A
     5    146.6      95.2    201  8  US-10-995-561-84658     Sequence 84658, A
     6     32.6      21.2    625  9  US-10-301-480-203835    Sequence 203835,
     7     32.6      21.2    625 10   US-10-301-480-817244     Sequence 817244,
     8     32.6      21.2    645  6  US-09-925-065A-103590   Sequence 103590,
     9     32.2      20.9    625  9  US-10-301-480-203834    Sequence 203834,
    10     32.2      20.9    625 10   US-10-301-480-817243     Sequence 817243,
    11     32.2      20.9    645  6  US-09-925-065A-103589   Sequence 103589,
c   12     31.8      20.6    662  6  US-09-925-065A-782496   Sequence 782496,
    13     31.6      20.5  24675 14   US-11-124-367A-5038      Sequence 5038, Ap
c   14     31.2      20.3    611  6  US-09-925-065A-370446   Sequence 370446,
c   15     31.2      20.3    611  6  US-09-925-065A-370447   Sequence 370447,
c   16     31.2      20.3    611  6  US-09-925-065A-370448   Sequence 370448,
c   17     31.2      20.3    627 10   US-10-301-480-440497     Sequence 440497,
c   18     31.2      20.3    627 10   US-10-301-480-440498     Sequence 440498,
c   19     31.2      20.3    627 10   US-10-301-480-440499     Sequence 440499,
c   20     31.2      20.3    627 10   US-10-301-480-1053906    Sequence 1053906,
c   21     31.2      20.3    627 10   US-10-301-480-1053907    Sequence 1053907,
c   22     31.2      20.3    627 10   US-10-301-480-1053908    Sequence 1053908,
    23     30.4      19.7    613  6  US-09-925-065A-757427   Sequence 757427,
    24     30.4      19.7 169495 14   US-11-121-086-61         Sequence 61, Appl
    25     30.2      19.6    996 14   US-11-098-686-9756       Sequence 9756, Ap
c   26     30.2      19.6 1457619 14   US-11-098-686-8739       Sequence 8739, Ap
    27       30      19.5   1931  9  US-10-301-480-94542     Sequence 94542, A
    28       30      19.5   1931  9  US-10-301-480-94543     Sequence 94543, A
    29       30      19.5   1931 10   US-10-301-480-707951     Sequence 707951,
    30       30      19.5   1931 10   US-10-301-480-707952     Sequence 707952,
c   31     29.8      19.4   1204  8  US-10-750-185-39545     Sequence 39545, A
c   32     29.8      19.4   1204  8  US-10-750-623-39545     Sequence 39545, A
    33     29.8      19.4   1400 14   US-11-136-527-6229       Sequence 6229, Ap
    34     29.8      19.4   1415 14   US-11-136-527-2133       Sequence 2133, Ap
    35     29.6      19.2    567 10   US-10-301-480-237751     Sequence 237751,
    36     29.6      19.2    567 10   US-10-301-480-851160     Sequence 851160,
    37     29.6      19.2    571  6  US-09-925-065A-143037   Sequence 143037,
c   38     29.6      19.2    726  8  US-10-750-185-50490     Sequence 50490, A
c   39     29.6      19.2    726  8  US-10-750-623-50490     Sequence 50490, A
    40     29.6      19.2   3885 11   US-11-079-463-930        Sequence 930, App
c   41     29.2      19.0    200 14   US-11-098-686-6769       Sequence 6769, Ap
c   42     29.2      19.0    499  6  US-09-925-065A-367162   Sequence 367162,
c   43     29.2      19.0    499  6  US-09-925-065A-367163   Sequence 367163,
c   44     29.2      19.0    507 10   US-10-301-480-437513     Sequence 437513,
c   45     29.2      19.0    507 10   US-10-301-480-437514     Sequence 437514,


                                ALIGNMENTS


RESULT 1
US-11-121-086-27
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 153142
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-27

  Query Match             100.0%;  Score 154;  DB 14;  Length 153142;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-39;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      87845 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 87904

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      87905 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 87964

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      87965 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 87998


RESULT 2
US-10-995-561-13467
; Sequence 13467, Application US/10995561
```

```
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13467
;   LENGTH: 16963
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13467

  Query Match             100.0%;  Score 154;  DB 8;  Length 16963;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-39;
  Matches  153;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      15958 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTASTCATGTCCCTAAA 16017

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16018 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 16077

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      16078 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 16111


RESULT 3
US-10-995-561-13513
; Sequence 13513, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13513
;   LENGTH: 40000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(40000)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13513

  Query Match             100.0%;  Score 154;  DB 8;  Length 40000;
  Best Local Similarity   99.4%;  Pred. No. 2.8e-39;
  Matches  153;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      38766 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTASTCATGTCCCTAAA 38825

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38826 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 38885

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
              ||||||||||||||||||||||||||||||||||
Db      38886 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 38919
```

```
RESULT 4
US-10-995-561-75740
; Sequence 75740, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75740
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-75740

  Query Match             95.2%;  Score 146.6;  DB 8;  Length 201;
  Best Local Similarity   99.3%;  Pred. No. 8.7e-38;
  Matches  146;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         55 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTASTCATGTCCCTAAA 114

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 174

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTC 147
              |||||||||||||||||||||||||||
Db        175 GGAGCTGGGGCAGAGGTCAGAGACCTC 201


RESULT 5
US-10-995-561-84658
; Sequence 84658, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84658
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-84658

  Query Match             95.2%;  Score 146.6;  DB 8;  Length 201;
  Best Local Similarity   99.3%;  Pred. No. 8.7e-38;
  Matches  146;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         55 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTASTCATGTCCCTAAA 114

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 174

Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTC 147
              |||||||||||||||||||||||||||
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Db        175 GGAGCTGGGGCAGAGGTCAGAGACCTC 201

RESULT 6
US-10-301-480-203835
; Sequence 203835, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 203835
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-203835

  Query Match             21.2%;  Score 32.6;  DB 9;  Length 625;
  Best Local Similarity   58.9%;  Pred. No. 1.7;
  Matches   56;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | ||||| ||
Db         45 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCCTGCAGA 104

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        105 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 139

RESULT 7
US-10-301-480-817244
; Sequence 817244, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817244
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-817244

  Query Match             21.2%;  Score 32.6;  DB 10;  Length 625;
  Best Local Similarity   58.9%;  Pred. No. 1.7;
  Matches   56;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | ||||| ||
Db         45 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCCTGCAGA 104

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        105 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 139

RESULT 8
US-09-925-065A-103590
; Sequence 103590, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103590
;   LENGTH: 645
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-103590

  Query Match             21.2%;  Score 32.6;  DB 6;  Length 645;
  Best Local Similarity   58.9%;  Pred. No. 1.8;
  Matches   56;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | ||||| ||
Db         65 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCCTGCAGA 124

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        125 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 159

RESULT 9
US-10-301-480-203834
; Sequence 203834, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 203834
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-203834

  Query Match             20.9%;  Score 32.2;  DB 9;  Length 625;
  Best Local Similarity   57.9%;  Pred. No. 2.4;
  Matches   55;  Conservative    1;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | |:||| ||
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```
Db         45 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCYTGCAGA 104

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        105 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 139


RESULT 10
US-10-301-480-817243
; Sequence 817243, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817243
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-817243

  Query Match             20.9%;  Score 32.2;  DB 10;  Length 625;
  Best Local Similarity   57.9%;  Pred. No. 2.4;
  Matches   55;  Conservative    1;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | |:||| ||
Db         45 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCYTGCAGA 104

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        105 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 139


RESULT 11
US-09-925-065A-103589
; Sequence 103589, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103589
;   LENGTH: 645
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-103589

  Query Match             20.9%;  Score 32.2;  DB 6;  Length 645;
  Best Local Similarity   57.9%;  Pred. No. 2.4;
  Matches   55;  Conservative    1;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGA 116
              | ||| ||| | | ||||  || ||  ||   |||| ||| || |  |  | |:||| ||
Db         65 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCYTGCAGA 124

Qy        117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151
               | | |    ||   |||||||| |      ||||
Db        125 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 159


RESULT 12
US-09-925-065A-782496/c
; Sequence 782496, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 782496
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-782496

  Query Match             20.6%;  Score 31.8;  DB 6;  Length 662;
  Best Local Similarity   51.8%;  Pred. No. 3.3;
  Matches   72;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70
              |||| ||| | |||| |||| |  |      |        | ||    ||||     |||
Db        141 TGCCACTGCACTCCAGACTGGATGACAGAGCGAGACTCAGTCTCTAAAAAAGAAAGAAAG 82

Qy         71 ATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGG 130
              |    ||  || ||| |||| || || | |  |  | ||| ||    || || |||  |||
Db         81 AAAAGAAAAAGAAAATAGCAGACTCATATCTGTGCCTTCCCCTGGATCTGGGACGTGGCC 22

Qy        131 CAGAGGTCAGAGACCTCTC 149
                   |   ||| |||| |
Db         21 AGAGAGAGGGAGCCCTCCC 3


RESULT 13
US-11-124-367A-5038
; Sequence 5038, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
```

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;   PRIOR FILING DATE: 2004-06-25
;   PRIOR APPLICATION NUMBER: US 60/599,554
;   PRIOR FILING DATE: 2004-08-09
;   NUMBER OF SEQ ID NOS: 34460
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5038
;    LENGTH: 24675
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-124-367A-5038

  Query Match             20.5%;  Score 31.6;  DB 14;  Length 24675;
  Best Local Similarity   55.5%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          2 TTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAA 61
              ||||    |||||||      ||     |       ||| | |||||  || |    | |
Db      18177 TTTGCAGACTGCCTCCCCTAGCCGGGAGGTCTGTTTTTCCGGCTACTGGTGACAAGTATA 18236

Qy         62 TGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCT 111
               |  |  || |||||| ||||||   ||| | ||||  | |||||  |||
Db      18237 AGTACTTACGTTGCAATCAGCAAGATGCACAAACACTCCTCTCCCACCCT 18286


RESULT 14
US-09-925-065A-370446/c
; Sequence 370446, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370446
;   LENGTH: 611
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-370446

  Query Match             20.3%;  Score 31.2;  DB 6;  Length 611;
  Best Local Similarity   57.0%;  Pred. No. 5;
  Matches   57;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          4 TGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATG 63
              | | |||   | |  |   ||| |||   | || |||||| || ||||   || ||| ||
Db        197 TTTTTGCAATCACACATTGCCAGACTATGCTAAGTTCAGCATAGTCATTCTCCAAAAGTG 138

Qy         64 GGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCT 103
              | || |||     |    || |||  | ||| |||  | |
Db        137 GACACACACACACACACACACACACAACACATACACACAT 98


RESULT 15
US-09-925-065A-370447/c
; Sequence 370447, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370447
;   LENGTH: 611
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-370447

  Query Match             20.3%;  Score 31.2;  DB 6;  Length 611;
  Best Local Similarity   57.0%;  Pred. No. 5;
  Matches   57;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          4 TGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATG 63
              | | |||   | |  |   ||| |||   | || |||||| || ||||   || ||| ||
Db        197 TTTTTGCAATCACACATTGCCAGACTATGCTAAGTTCAGCATAGTCATTCTCCAAAAGTG 138

Qy         64 GGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCT 103
              | || |||     |    || |||  | ||| |||  | |
Db        137 GACACACACACACACACACACACACAACACATACACACAT 98


Search completed: April 18, 2006, 15:39:40
Job time : 95.5846 secs
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                         GenCore version 5.1.7
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         April 18, 2006, 12:23:43 ; Search time 32.8522 Seconds
                                           (without alignments)
                                           8332.600 Million cell updates/sec

Title:          US-09-884-901A-8
Perfect score:  154
Sequence:       1 gtttgtgtgctgcctctgaa..........ggtcagagacctctctgggc 154

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:        2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
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                5:  /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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                9:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

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Result          Query
  No.   Score  Match Length DB  ID                       Description
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     1    154  100.0    774  3  US-08-221-767-1           Sequence 1, Appli
     2     82   53.2     90  3  US-09-001-039B-61         Sequence 61, Appl
     3     82   53.2     90  3  US-09-001-039B-65         Sequence 65, Appl
c    4     78   50.6     82  3  US-09-001-039B-67         Sequence 67, Appl
c    5     77   50.0     82  3  US-09-001-039B-63         Sequence 63, Appl
c    6     74   48.1     78  3  US-09-001-039B-64         Sequence 64, Appl
c    7     74   48.1     78  3  US-09-001-039B-68         Sequence 68, Appl
     8     70   45.5     70  3  US-09-001-039B-66         Sequence 66, Appl
     9     69   44.8     70  3  US-09-001-039B-62         Sequence 62, Appl
c   10     31   20.1   2018  3  US-09-799-451-433         Sequence 433, App
    11     31   20.1 113379  3  US-09-949-016-17561       Sequence 17561, A
    12     31   20.1 113379  3  US-09-949-016-17562       Sequence 17562, A
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    14   30.2   19.6  80706  3  US-09-949-016-15347       Sequence 15347, A
c   15     30   19.5    658  3  US-09-669-751-144         Sequence 144, App
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    17   29.2   19.0    606  3  US-09-533-559-3897        Sequence 3897, Ap
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c   19   29.2   19.0  86213  3  US-09-949-016-17240       Sequence 17240, A
c   20   29.2   19.0  86213  3  US-09-949-016-17241       Sequence 17241, A
c   21   29.2   19.0  86213  3  US-09-949-016-17242       Sequence 17242, A
c   22   29.2   19.0  86213  3  US-09-949-016-17243       Sequence 17243, A
    23     29   18.8    748  3  US-09-270-767-12592       Sequence 12592, A
c   24   28.8   18.7    401  3  US-09-513-999C-28004      Sequence 28004, A
    25   28.8   18.7   1762  2  US-08-105-483-300         Sequence 300, App
    26   28.8   18.7   1762  2  US-08-709-209-300         Sequence 300, App
    27   28.8   18.7   1762  2  US-08-458-101-300         Sequence 300, App
c   28   28.8   18.7   1881  3  US-09-949-016-2351        Sequence 2351, Ap
c   29   28.8   18.7  14094  3  US-09-949-016-14093       Sequence 14093, A
c   30   28.8   18.7 126237  3  US-09-949-016-16674       Sequence 16674, A
c   31   28.8   18.7 126237  3  US-09-949-016-16675       Sequence 16675, A
c   32   28.6   18.6 421491  3  US-09-949-016-12805       Sequence 12805, A
c   33   28.6   18.6 421494  3  US-09-949-016-14060       Sequence 14060, A
c   34   28.4   18.4    385  3  US-09-313-294A-5044       Sequence 5044, Ap
    35   28.4   18.4 102053  3  US-09-949-016-13025       Sequence 13025, A
c   36   28.4   18.4 192956  3  US-09-949-016-14382       Sequence 14382, A
c   37   28.2   18.3   3068  2  US-07-984-044A-3         Sequence 3, Appli
c   38   28.2   18.3   3068  2  US-08-458-393-3           Sequence 3, Appli
c   39     28   18.2    585  3  US-09-621-976-16302       Sequence 16302, A
c   40     28   18.2  20040  3  US-09-949-002-610         Sequence 610, App
c   41     28   18.2  20041  3  US-09-949-002-718         Sequence 718, App
c   42     28   18.2  23928  3  US-09-949-016-12392       Sequence 12392, A
c   43     28   18.2  23928  3  US-09-949-016-16315       Sequence 16315, A
c   44     28   18.2 193303  3  US-09-497-855A-37         Sequence 37, Appl
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                                ALIGNMENTS


RESULT 1
US-08-221-767-1
; Sequence 1, Application US/08221767
; Patent No. 6268212
;  GENERAL INFORMATION:
;    APPLICANT:  Simonet, William S.
;    APPLICANT:  Lichenstein, Henri S.
;    APPLICANT:  Lyons, David E.
;    TITLE OF INVENTION:  Tissue Specific Transgene Expression
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc., U.S. Patent Operations/NAO
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,767
;      FILING DATE:
;      CLASSIFICATION:  800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-221-767-1

  Query Match             100.0%;  Score 154;  DB 3;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-40;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 140

Qy         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 120
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Db        141 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTT 200
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Qy        121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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Db        201 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 234


RESULT 2
US-09-001-039B-61
; Sequence 61, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  90 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-61

  Query Match             53.2%;  Score 82;  DB 3;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-17;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 3
US-09-001-039B-65
; Sequence 65, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  90 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-65

  Query Match             53.2%;  Score 82;  DB 3;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-17;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68

Qy         61 ATGGGCAAACATTGCAAGCAGC 82
              ||||||||||||||||||||||
Db         69 ATGGGCAAACATTGCAAGCAGC 90


RESULT 4
US-09-001-039B-67/c
; Sequence 67, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
```

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-67

  Query Match             50.6%;  Score 78;  DB 3;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-16;
  Matches   78;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         75 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 23

Qy        135 GGTCAGAGACCTCTCTGG 152
              ||||||||||||||||||
Db         22 GGTCAGAGACCTCTCTGG 5


RESULT 5
US-09-001-039B-63/c
; Sequence 63, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-63

  Query Match             50.0%;  Score 77;  DB 3;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-16;
  Matches   77;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         75 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 23

Qy        135 GGTCAGAGACCTCTCTG 151
              |||||||||||||||||
Db         22 GGTCAGAGACCTCTCTG 6


RESULT 6
US-09-001-039B-64/c
; Sequence 64, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
```

```
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  64:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  78 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-64

  Query Match             48.1%;  Score 74;  DB 3;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-15;
  Matches   74;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 15

Qy         61 ATGGGCAAACATTG 74
              ||||||||||||||
Db         14 ATGGGCAAACATTG 1


RESULT 7
US-09-001-039B-68/c
; Sequence 68, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  78 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-68

  Query Match             48.1%;  Score 74;  DB 3;  Length 78;
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  Best Local Similarity   100.0%;  Pred. No. 8.8e-15;
  Matches   74;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 15

Qy         61 ATGGGCAAACATTG 74
              ||||||||||||||
Db         14 ATGGGCAAACATTG 1


RESULT 8
US-09-001-039B-66
; Sequence 66, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  66:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  70 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-66

  Query Match             45.5%;  Score 70;  DB 3;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-13;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAG 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAG 60

Qy        143 ACCTCTCTGG 152
              ||||||||||
Db         61 ACCTCTCTGG 70
```

```
RESULT 9
US-09-001-039B-62
; Sequence 62, Application US/09001039B
; Patent No. 6818439
;  GENERAL INFORMATION:
;    APPLICANT:  Jolly, Douglas J.
;    APPLICANT:  Chang, Stephen M.W.
;    APPLICANT:  Respess, James G.
;    APPLICANT:  DePolo, Nicholas J.
;    APPLICANT:  Hsu, David Chi-Tang
;    APPLICANT:  Ibanez, Carlos E.
;    APPLICANT:  Greengard, Judith
;    APPLICANT:  Lee, Will
;    TITLE OF INVENTION:  METHODS FOR ADMINISTRATION OF
;    TITLE OF INVENTION:  RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
;    TITLE OF INVENTION:  OF HEMOPHILIA AND OTHER DISORDERS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed Intellectual Property Law Group
;      STREET:  701 Fifth Avenue, Suite 6300
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,039B
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  1155.005 / 930049.441C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-001-039B-62

  Query Match             44.8%;  Score 69;  DB 3;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-13;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAG 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAG 60

Qy        143 ACCTCTCTG 151
              |||||||||
Db         61 ACCTCTCTG 69


RESULT 10
US-09-799-451-433/c
; Sequence 433, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
```

```
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Yamazaki, Victoria
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Reena
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6783969el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 803
;  CURRENT APPLICATION NUMBER: US/09/799,451
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 433
;   LENGTH: 2018
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1746)
US-09-799-451-433

  Query Match             20.1%;  Score 31;  DB 3;  Length 2018;
  Best Local Similarity   62.0%;  Pred. No. 3.5;
  Matches   49;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         33 CAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAA 92
              || | ||  ||  | ||||||| | || |  ||||  |  ||  ||  ||   | |||
Db       1917 CACAGTTGCGCTCATTCATGTCTCGAATAGCGGCATGCTCTGGGAGTCGCTGTCTGCAGT 1858

Qy         93 CACACAGCCCTCCCTGCCT 111
              ||| |||||| ||  ||||
Db       1857 CACCCAGCCCCCCTGGCCT 1839


RESULT 11
US-09-949-016-17561
; Sequence 17561, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17561
;   LENGTH: 113379
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17561

  Query Match             20.1%;  Score 31;  DB 3;  Length 113379;
  Best Local Similarity   56.3%;  Pred. No. 15;
  Matches   58;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         12 GCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACA 71
              |||| ||||  ||   ||||| |    |||| | | | || |     |||  |||| |
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```
Db      67313 GCCTTTGAAACCCTTCCTGAATAGTTGTCAGACAATTGATTTTGAATAAAATGGCACAAT 67372

Qy         72 TTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
                |||||||  || |  |  ||  |  ||    | |||   ||||
Db      67373 AGGCAAGCAACATAATGGAACTAGTCAAAAGTACCTAAGTGCT 67415


RESULT 12
US-09-949-016-17562
; Sequence 17562, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17562
;   LENGTH: 113379
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17562

  Query Match             20.1%;  Score 31;  DB 3;  Length 113379;
  Best Local Similarity   56.3%;  Pred. No. 15;
  Matches   58;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         12 GCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACA 71
              |||| ||||  ||   ||||| |    |||| | | | || |     |||  |||| |
Db      67313 GCCTTTGAAACCCTTCCTGAATAGTTGTCAGACAATTGATTTTGAATAAAATGGCACAAT 67372

Qy         72 TTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCT 114
                |||||||  || |  |  ||  |  ||    | |||   ||||
Db      67373 AGGCAAGCAACATAATGGAACTAGTCAAAAGTACCTAAGTGCT 67415


RESULT 13
PCT-US93-06251-23/c
; Sequence 23, Application PC/TUS9306251
;  GENERAL INFORMATION:
;    APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;    TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;    TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06251
;      FILING DATE:  19930630
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8586
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11558 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-23

  Query Match             19.7%;  Score 30.4;  DB 6;  Length 11558;
  Best Local Similarity   51.5%;  Pred. No. 10;
  Matches   70;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy          9 GCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAA 68
              ||  |||| ||  |||    ||  |   ||||||    | |  | |||| |  || ||
Db       9728 GCCCCCTCCGAGCTCCGACTTGGGCCCTCTTCAGTTCCCACTGGACCCTGATTTGAGCTG 9669

Qy         69 ACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGG 128
               |  || ||  |||  | | |  | || | |  | |   | |    |  |  ||||  |
Db       9668 GCTCTGGAAATAGCTGAGAACCCAGACGCGGGACGCAGGGGCAAGGGCTCAAGGAGGAGA 9609

Qy        129 GGCAGAGGTCAGAGAC 144
              | |||||   |||| |
Db       9608 GTCAGAGTCAAGAGGC 9593


RESULT 14
US-09-949-016-15347
; Sequence 15347, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15347
;   LENGTH: 80706
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(80706)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15347

  Query Match             19.6%;  Score 30.2;  DB 3;  Length 80706;
  Best Local Similarity   55.1%;  Pred. No. 24;
  Matches   59;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy         47 CTCATGTCCCTAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCC 106
              | | |||||||   |||    |  |   |   |||| | | ||  | |  ||||||   |
Db      35087 CACCTGTCCCTGGGATGCAGGAGAACATCTTCCAGCCATCTGCCCAGAGCCAGCCCGAGC 35146

Qy        107 TGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGG 153
               ||  || |     ||||| ||||  | |  | |  | ||||||| |
Db      35147 AGCTGGCAGCAGGAGGAGCCGGGGATGTGTGCTGTTATCTCTCTGCG 35193


RESULT 15
```

```
US-09-669-751-144/c
; Sequence 144, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
;  APPLICANT:  Greenspan, Ralph J.
;  TITLE OF INVENTION:  Methods for Identifying Compounds for
;  TITLE OF INVENTION:  Motion Sickness, Vertigo and Other Disorders Related to
;  TITLE OF INVENTION:  Balance and the Perception of Gravity
;  FILE REFERENCE:  P-NI 3864
;  CURRENT APPLICATION NUMBER: US/09/669,751
;  CURRENT FILING DATE:  2000-09-26
;  PRIOR APPLICATION NUMBER:  US 60/168,579
;  PRIOR FILING DATE:  1999-12-02
;  NUMBER OF SEQ ID NOS:  261
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 658
;   TYPE: DNA
;   ORGANISM: Drosophila
US-09-669-751-144

  Query Match             19.5%;  Score 30;  DB 3;  Length 658;
  Best Local Similarity   53.4%;  Pred. No. 5;
  Matches   63;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy         10 CTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAA 69
              |||  |||| |    |  ||| |  |  ||| || |  |  | | | | | ||  | |||
Db        392 CTGATTCTGCATCAGATTCTGCATCAGATTCTGCATCATATTCTGCATCAGATTCGGAAA 333

Qy         70 CATTGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTG 127
              |||    | ||  |  | ||||   |  || |  |   ||| | |||  || |||| |
Db        332 CATCTTCATCAATAGTCTGCAAGGGCTTAGACTGCTTCGCCAGTTGATTTTTGAGCCG 275

Search completed: April 18, 2006, 12:30:28
Job time : 34.8522 secs
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